

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Waeber T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carlinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
BL Nature 409:685-690(2001).
CC -!- FUNCTION: Cooperates with LY96 and TLR6 to mediate the innate
CC immune response to bacterial lipoproteins and other microbial cell
CC wall components. Acts via MyD88 and TRAF6, leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response. May
CC also promote apoptosis in response to lipoproteins (By
CC similarity).
CC -!- SUBUNIT: Binds LY96 and TLR6 via the extracellular domain. Binds
CC MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosome.
CC -!- TISSUE SPECIFICITY: Detected in a macrophage cell line, smooth
CC muscle, lung, spleen, thymus, brain and adipose tissue.
CC -!- PM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 1 TIR domain.
CC -!- SIMILARITY: Contains 16 leucine-rich (LRR) repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF185284; AAF04277.1; -;
CC DR EMBL; AF124741; AAD46481.1; -;
CC DR EMBL; AF216289; AAF28345.1; -;
CC DR EMBL; AF165189; AAD49335.1; -;
CC DR EMBL; AK005043; BAB23770.1; -;
CC DR HSP; O60603; 1FYW
CC MGD; MGI:1346060; Tlr2.
CC InterPro; IPR004075; IL1_receptor1.
CC DR InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_Cterm.
CC DR InterPro; IPR003591; LRR_Typ.
CC DR InterPro; IPR000157; TIR.
CC Pfam; PF00560; LRR; 6.
CC DR Pfam; PF01463; LRRCT; 1.
CC Pfam; PF01582; TIR; 1.
CC DR PRINTS; PR01537; INTRLNRIIP.
CC DR PRINTS; PR00019; LEURICHRPT.
CC DR SMART; SM00369; LRR_TYP; 2.
CC DR SMART; SM00082; LRRCT; 1.
CC DR SMART; SM00255; TIR; 1.
CC DR PROSITE; PS0104; TIR; 1.
CC KW Receptor; Immune response; Inflammatory response; Signal;
CC Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL. RECEPTOR 2.
FT CHAIN 25 784 TOLL-LIKE RECEPTOR 2.
FT DOMAIN 25 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 608 POTENTIAL.
FT DOMAIN 609 784 CYTOPLASMIC (POTENTIAL).
FT REPEAT 51 74 LRR 1.
FT REPEAT 75 98 LRR 2.

FT REPEAT	99	122	LRR 3.
FT REPEAT	124	147	LRR 4.
FT REPEAT	173	196	LRR 5.
FT REPEAT	221	244	LRR 6.
FT REPEAT	276	300	LRR 7.
FT REPEAT	335	358	LRR 8.
FT REPEAT	359	384	LRR 9.
FT REPEAT	386	411	LRR 10.
FT REPEAT	412	436	LRR 11.
FT REPEAT	438	456	LRR 12.
FT REPEAT	457	476	LRR 13.
FT REPEAT	477	500	LRR 14.
FT REPEAT	502	521	LRR 15.
FT REPEAT	522	548	LRR 16.
FT DOMAIN	639	784	TIR.
FT CARBOHYD	147	147	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN	681	681	P-SH: ABOLISHES MYD88-BINDING AND RESPONSE TO MICROBIAL CELL WALL COMPONENTS.
FT CONFLICT	59	59	L -> P (IN REF. 5).
FT CONFLICT	82	82	I -> M (IN REF. 5).
FT SEQUENCE	784 AA;	89448 MW;	606D56BF85F320A2 CRC64;

Query Match 7.1%; Score 130.5; DB 1; Length 784;
Best Local Similarity 21.5%; Pred. No. 0.015;
Matches 70; Conservative 52; Mismatches 11; Indels 93; Gaps 16;

Qy	46	NLEPF--LKRVD-----ADADPRQY-ADTVKALR-VRRITVGAQVP--AQLL 87
Db	158	NVTFSEIRIDFAGLTSLNELETKALSLRNYQSLSKIRDIHLLHLHLSAFLLEIF 217
Qy	88	VGALRVLAYSRLEKLTLEDLKITCTMPPLPLEATGLALSSRLRNVSWATGRSW--LAEL 145
Db	218	ADILSSVRYLELRDTNLRQFS---PLPVDVSSPMKKLAERG-SVLTDSEFNELKL 272
Qy	146	QOWL-----KPG-----LKVLISIAQAHSPAF----- 166
Db	273	LRYLELSEVEFDCTUNGGLGDFNPSSDVVSELGKVTETVIRLHLIPQVLYFDLSTVY 332
Qy	167	-----SYEQVRAF-----PALTSLDSDNPGGLGERGLMAALCPHKFPATQN 207
Db	333	SLLEKVKRITVENSKEVFLVPCFSFQHLKSLFELDSENL-MVEEYKNSACKGAWPSLQT 391
Qy	208	LALRNTGMET--PTGVCAALAAAGVQHSKLDLSHNSLRATVNPSPAPRCMWSALNSLNS 265
Db	392	LVLSQLHLSRMQKTG---EILLTLKNTSLDISN-----TFHPMPDSCQWPKRMFLNLS 444
Qy	266	PAGLEQVPGKLPKLRVLDLSCNPLN 291
Db	445	STGIRVVKTCIPQTLVLDVSNNNLD 470

Search completed: October 4, 2004, 16:54:51

Job time : 30 secs

RESULT 13
 TL22 CHICK STANDARD; PRT; 781 AA.
 AC Q9DGB6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toll-like receptor 2 type 2 precursor.
 GN TLR2-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21601652; PubMed=11590137;
 RA Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,
 Toyoshima K., Seya T.;
 RT "Molecular cloning and functional characterization of chicken Toll-
 like receptors. A single chicken Toll covers multiple molecular
 patterns";
 RL J. Biol. Chem. 276:47143-47149(2001).
 CC -!- FUNCTION: Participates in the innate immune response to microbial
 agents. Acts via Myd88 and TRAF6, leading to NF-kappa-B
 activation, cytokine secretion and the inflammatory response.
 CC Mediates the response to mycoplasma macrophage-activating
 lipopeptide-2kD (MALP-2).
 CC -!- SUBUNIT: Binds Myd88 via their respective TIR domains. Binds TLR6
 via their respective extracellular domains (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Highly expressed in ovary. Also detected in
 brain, heart, lung, liver, spleen and kidney, and at low levels in
 gizzard, muscle, testis and proventriculus.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -!- SIMILARITY: Contains 1 TIR domain.
 CC -!- SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
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 or send an email to license@isb-sib.ch).

 DR EMBL; AB046533; BAB16842.1; --
 DR HSBP; O60603; 1FW.
 DR InterPro; IPR004075; IL1_receptor1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR Cterm.
 DR InterPro; IPR003591; LRR typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 9.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRLNIRIF.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR Receptor; Immune response; Inflammatory response; Signal;
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 781 TOLL-LIKE RECEPTOR 2 TYPE 2.
 FT DOMAIN 25 595 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 586 606 POTENTIAL.
 FT DOMAIN 607 781 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.

FT REPEAT 100 122 LRR 3.
 FT REPEAT 124 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 173 195 LRR 6.
 FT REPEAT 356 381 LRR 7.
 FT REPEAT 383 409 LRR 8.
 FT REPEAT 410 433 LRR 9.
 FT REPEAT 435 453 LRR 10.
 FT REPEAT 454 473 LRR 11.
 FT REPEAT 474 497 LRR 12.
 FT REPEAT 499 518 LRR 13.
 FT DOMAIN 636 781 TIR.
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 781 AA; 89094 MW; 7211B399C6320454 CRC64;
 Query Match 7.3%; Score 135; DB 1; Length 781;
 Best Local Similarity 21.9%; Pred. No. 0.0064;
 Matches 77; Conservative 62; Mismatches 137; Indels 76; Gaps 15;
 Qy 18 NFSEPQDMSEAFQCVSAVEVEIHAGLNLEPFLKRVDA-DADPROYADTVKALRVRLT 76
 Db 184 NLSQVEPGSLSKIRKINHMIISI-----RRIDVFSAVIRDLLHSAIMLDVRKL- 231
 Qy 77 VGAQVPAQLLVGALRVLAYSLKELTELDLKIT-GTVPPLPLEATGL-ALSSLRNRVS 134
 Db 232 --AFSVEKTLQ--LRIMSSFAKISLKQCLFTDAIVPEIVSLGMPKLMVEVMKDC 287
 Qy 135 WATGRSLAELQWLKPLKVLSTQAHPAF-----SYQVRAF- 174
 Db 288 LLGTGKWKQIHANQSOSLRILTNIENLSIBEFYLTDLQSVLDLILFRKVTVENTKVL 347
 Qy 175 -----PALTSLDLSDNPGLGEMALCPHKFPAIQNLALRNTGMEPTGVCAL 225
 Db 348 VPCKLSQHLISLEYLDLSANL-LGDQSLHSACGAWPSLQTLNLSNLSL-----SDL 399
 Qy 226 AAGV-----QPHSLDLSHNSLRATVNPSPAPRCWSSALNSLNSLNSLNSLNSLNSL 279
 Db 400 KMTCKSLFHLNENLLDISENNF-----GEIPDMCEPENLKYLNLSSTQIPKLTCTPIST 455
 Qy 280 LRVLDLSCNLRNAPQPD---ELPEVNLTLDGNPF--LVPGTALPHEGSMN 326
 Db 456 LEVLDSANNLIQ-----DFGLQLPLKELYLTKNHLKTLPEATDIPNLVAMS 502

RESULT 14
 TLR2 CRIGR STANDARD; PRT; 784 AA.
 AC Q9R1F8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Toll-like receptor 2 precursor.
 GN TLR2.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovarian carcinoma;
 RX MEDLINE=99288048; PubMed=10358136;
 RA Heine H., Kirschning C.J., Lien E., Monks B.G., Rothe M.,
 RA Golenbock D.T.;
 RT "Cells that carry a null allele for Toll-like receptor 2 are capable
 of responding to endotoxin.";

283 LDLSNRLNRAPQP-DELFEVDNTLDGNPLVPCTALPHEGSMNS 327
||| ||: |: | : | : | : | : | :
453 LDLHNNRIMSPKDVTHLQALQELNVASNSL----TDLPGCGARSS 494

RESULT 12
PSKR DAUCA STANDARD; PRT; 1021 AA.
AC Q8LPB4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phytosulfokine receptor precursor (EC 2.7.1.37) (Phytosulfokine LRR
receptor kinase).
DE PSKR.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Apiales; Apiaceae; Apioidae; Scandiceae; Daucinae;
OC Daucus.
NCBI_TaxID=4039;
[1]
SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND GLYCOSYLATION.
RX MEDLINE=22025707; PubMed=12029134;
RA Matsubayashi Y., Ogawa M., Morita A., Sakagami Y.;
RT "An LRR receptor kinase involved in perception of a peptide plant
RT hormone, phytosulfokine."
RL Science 296:1470-1472(2002).
CC -|- FUNCTION: Receptor with a serine/threonine-protein kinase
CC activity. Regulates, in response to phytosulfokine binding, a
CC signaling cascade involved in plant cell differentiation,
CC organogenesis and somatic embryogenesis.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane (By
CC similarity).
CC -|- TISSUE SPECIFICITY: Expressed ubiquitously in leaf, apical
CC meristem, hypocotyl and root.
CC -|- PTM: N-glycosylated.
CC -|- MISCELLANEOUS: A 36 amino-acid island is present in the 18th
CC leucine-rich repeat. An island domain has also been found among
CC the extra-cellular LRRs of the brassinosteroid receptor BRI1 and
CC has been shown to be critical for its function.
CC -|- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -|- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.

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EMBL: AB060167; BAC00995.1; --
DR InterPro; IPR001631; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TY_KC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Kinase; Serine/threonine-protein kinase; Receptor;
ATP-binding; Repeat; Leucine-rich repeat; Signal; Transmembrane;
KW Glycoprotein.

```
Db 227 PREISKLHAKLDSYNPLKCSIPKSGFGLHNLILNLSVAELIGIPPELGNCKSLKS 286
Qy 283 LDLSNCRNLRAPODELPEV-----DNLTIDGNPFPLVPG 316
Db 287 LMLSFNLS-GPLPLESEIPLTFSAERNQLSGSLPSWGWKVKVLSLLANNRF---S 342
Qy 317 TALPHE-----GSMNSGVVP--ACARSTL-SVGVSGLV 347
Db 343 GEIPHEIEDCPMLKHLSLASNLGSGSIPRELCGSGSLEAIDLSGNLL 389

RESULT 11
TLRI MOUSE
ID TLRI MOUSE STANDARD; PRT; 795 AA.
AC Q9BPQ1; Q9EPW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like)
DE (TIR).
GN TLR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Macrophage;
RX MEDLINE=20558581; PubMed=11095740;
RA Ozinsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D.,
RA Wilson C.B., Schroeder L., Aderem A.;
RA "The repertoire for pattern recognition of pathogens by the innate
RT immune system is defined by cooperation between Toll-like
RT receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771(2000).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=20571875; PubMed=11123271;
RA Hajjar A.M., O'Mahony D.S., Ozinsky A., Underhill D.M., Aderem A.,
RA Klebanoff S.J., Wilson C.B.;
RA "Functional interactions between Toll-like receptor (TLR) 2 and TLR1
RT or TLR6 in response to phenol-soluble modulins.";
RL J. Immunol. 166:15-19(2001).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RA Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;
RA "Cloning of Mus musculus Toll-like receptor 1.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (By similarity).
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 1 TIR domain.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
CC
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CC
CC EMBL; AY009154; ANG37302.1; --
```

```
DR EMBL; AF316985; AAC35062.1; -.
DR HSP; O60603; IPYV.
DR MGD; MGI:1341295; Tlr1.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0045335; C:phagocytic vesicle; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0004888; F:transmembrane receptor activity; NAS.
DR GO; GO:0042497; F:triacylated lipoprotein binding; NAS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
DR GO; GO:0042116; P:macrophage activation; NAS.
DR GO; GO:0042495; P:perception of triacylated bacterial lipopro. .; NAS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. .; IMP.
DR GO; GO:0042535; P:positive regulation of tumor necrosis facto. .; IMP.
DR InterPro; IPR004075; ILL_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNKIR1F.
DR PRINTS; SM00082; LRRCT; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SMO0255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 25
FT CHAIN 26 795
FT DOMAIN 26 582
FT TRANSMEM 583 603
FT DOMAIN 604 795
FT REPEAT 46 70
FT REPEAT 71 94
FT REPEAT 96 116
FT REPEAT 117 140
FT REPEAT 140 140
FT REPEAT 374 397
FT REPEAT 400 427
FT REPEAT 447 470
FT REPEAT 471 494
FT REPEAT 496 515
FT REPEAT 638 782
FT DOMAIN 38 38
FT CARBOHYD 59 59
FT CARBOHYD 88 88
FT CARBOHYD 140 140
FT CARBOHYD 166 166
FT CARBOHYD 251 251
FT CARBOHYD 296 296
FT CARBOHYD 333 333
FT CARBOHYD 432 432
FT CONFLICT 88 88
SQ SEQUENCE 795 AA; 90672 MW; 855356429872D232 CRC64;
Query Match 7.5%; Score 138; DB 1; Length 795;
Best Local Similarity 21.3%; Pred. No. 0.0038;
Matches 61; Conservative 50; Mismatches 113; Indels 62; Gaps 9;
Qy 68 KALRVRLTVGAQVPAQLLVGLARVLAYSRLKLTLEDLKITGTMTPLPLEATGLALSS 127
Db 245 KNLKLSNLTLNNVETWNSFINLIQIVMHTPVKYSINVKLQGL-----A 291
Qy 128 LRLRVSWATGSRWLAELQWLKPLKVLSTAQHSFAFSYEQVRAFPALTSLDLSDNPG 187
Db 292 FRMFNYS-----DTSLKALSIHQVTVDFSPSPQSYIYSIFANMNI-QNFT 335
Qy 188 LGERGLMAALCP-----HKFPAIOMLALNTGWTPTGCA 223
Db 336 MSGTHVMHMLCPQSQVSPPLHVDFDTNLTDMVFDKCRNLVRLKTLKLNQKLNLEIIL 395
Qy 224 ALAAGVQPHSLDLSHNSLRATVNPSPAPRCWSSALNSLNLSFAGLE-QVPGKLPKLRV 282
Db 396 T-SAKWTSIQKLDLSQNSLR--YSDGGIPCAWTQSLVLLVSSNMLTGSVFRCLPPKVKV 452
```

RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
 RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., J.,
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Böhret A., Miller B., Marra M.A.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Voickaert G., Wambutt R., Dueterhoeft A., Stiekema W., Pohl T.,
 RA Entian K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
 RA Ransperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,
 RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feidenschmidt M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
 RA Schueller C., Zaccaria P., Meves H.-W., Bevan M., Franz P.F.,
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RT thaliana",
 RL Nature 408:923-926(2000).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity required for the specification of the correct number of
 CC male archesporial initials and for the subsequent specification of
 CC tapetal and middle cell layer identities. In seeds, required for
 CC enhancing cell size and the rate of embryonic development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- TISSUE SPECIFICITY: Present in young buds, open flowers and
 CC siliques but absent from mature leaves and roots. Strongly
 CC expressed in the young organ primordia, and as the anthers and
 CC ovules developed, became focused in the microsporangia and in the
 CC distal and chalazal regions of the ovule. In cv. Landsberg erecta,
 CC only expressed in the anthers of young floral buds.
 CC -!- DEVELOPMENTAL STAGE: Expressed during the differentiation of
 CC microsporocytes and tapetal cells. Also expressed in the meiocytes
 CC and young pollen grains until pollen mitosis II.
 CC -!- PTM: Autophosphorylates in vitro.
 CC -!- MISCELLANEOUS: Some ecotypic variation may occur: in cv.
 CC Landsberg erecta, meiocytes of a null mutant fail to undergo
 CC cytokinesis while in cv. C24, cytokinesis clearly takes place,
 CC with the mutant meiocytes degenerating shortly after the tetrad
 CC stage.
 CC -!- MISCELLANEOUS: In cv. C24, the gene is expressed in the young
 CC ovular primordia, but the protein is not present in these organs.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 29 leucine-rich (LRR) repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR ENBL; AJ496433; CAD2912.1; -
 DR ENBL; AJ488154; CAD32463.1; -
 DR ENBL; AL163652; CAB87284.1; -
 DR PIR; T48499; T48499.
 DR Germline; 181167; -
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00560; LRR; 19.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Kinase; Serine/threonine-protein kinase; Receptor;
 KW ATP-binding; Repeat; Signal; Transmembrane; Leucine-rich repeat;

KW Phosphorylation; Meiosis.
 FT SIGNAL 1 18
 FT CHAIN 19 1192
 FT
 FT REPEAT 64 87
 FT REPEAT 88 112
 FT REPEAT 114 135
 FT REPEAT 136 160
 FT REPEAT 162 185
 FT REPEAT 187 209
 FT REPEAT 233 256
 FT REPEAT 258 280
 FT REPEAT 281 305
 FT REPEAT 307 327
 FT REPEAT 328 351
 FT REPEAT 352 376
 FT REPEAT 378 399
 FT REPEAT 400 424
 FT REPEAT 426 447
 FT REPEAT 449 470
 FT REPEAT 471 495
 FT REPEAT 497 518
 FT REPEAT 519 543
 FT REPEAT 545 569
 FT REPEAT 579 602
 FT REPEAT 603 626
 FT REPEAT 627 651
 FT REPEAT 653 674
 FT REPEAT 676 698
 FT REPEAT 699 723
 FT REPEAT 725 746
 FT REPEAT 747 770
 FT REPEAT 771 796
 FT TRANSMEM 828 848
 FT DOMAIN 917 1192
 FT NP BIND 923 931
 FT BINDING 945 945
 FT ACT SITE 1043 1043
 FT MUTAGEN 4 4
 FT MUTAGEN 104 104
 FT MUTAGEN 1185 1185
 FT CONFLICT 131 132
 FT CONFLICT 138 138
 FT CONFLICT 155 155
 FT CONFLICT 209 209
 FT CONFLICT 258 258
 FT CONFLICT 273 273
 FT CONFLICT 325 325
 FT CONFLICT 347 347
 FT CONFLICT 572 572
 FT CONFLICT 852 852
 FT CONFLICT 866 866
 FT CONFLICT 1075 1075
 SQ SEQUENCE 1192 AA; 129799 MW; D02C8B8F6B09F7D CRC64;

Query Match 7.7%; Score 142; DB 1; Length 1192;
 Best Local Similarity 23.9%; Pred. No. 0.0031;
 Matches 83; Conservative 48; Mismatches 116; Indels 100; Gaps 14;

QY 77 V GAAQVPAQLLVGAL--RVLAYSRKLKLTLEDKITGTMP--LPLEATGLALS 126
 Db 67 VNSLSLPSLSLRGQIPKETSLSKLNKRLCLAGNQFGSKIPETIWNKHLQTLDSGNSLT 126
 QY 127 SLRLRVSWATGRSWLAELQQLWPKGLKVLISIAQAHSFAFSYEQVRAFPALTSLDSDNP 186
 Db 127 GLLP--LLESELPLQLLYLDLSDNHFFSSLPSPFFI---SLPALSLSDVSNNS 173
 QY 187 GLGERGLMAALCPHKPFAITONLALRNTGMTPTG-----VCAALAAA-----GVQ 231
 Db 174 LSGE-----IPPETGKLSNLYNGLNSFGQIPSEIGNISLLKNFAAPSCFFNGPL 226
 QY 232 PH-----SLDLSHNSLRATVNPSPAPRCMSSALNSLNSLGFAGLEQVPKGLPAKLRY 282

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EMBL; AY045573; AAK91868.1; -
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 4.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNRI1F.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 18
FT CHAIN 19 784
FT DOMAIN 19 587
FT TRANSMEM 588 608
FT DOMAIN 609 784
FT REPEAT 51 74
FT REPEAT 75 98
FT REPEAT 99 122
FT REPEAT 124 147
FT REPEAT 149 172
FT REPEAT 173 196
FT REPEAT 221 244
FT REPEAT 359 384
FT REPEAT 386 411
FT REPEAT 412 436
FT REPEAT 438 456
FT REPEAT 457 476
FT REPEAT 477 499
FT REPEAT 501 521
FT REPEAT 521 544
FT DOMAIN 544 784
FT CARBOHYD 114 114
FT CARBOHYD 199 199
FT CARBOHYD 414 414
FT CARBOHYD 442 442
FT SEQUENCE 784 AA; 89987 MW; 3386E36DB32CAB3E CRC64;

Query Match 7.8%; Score 144; DB 1; Length 784;
Best Local Similarity 21.5%; Pred. No. 0.0013;
Matches 83; Conservative 62; Mismatches 141; Indels 100; Gaps 16;

QY 4 EPCLEDEPRVCNFSFQPDWSEAFQCVSAVEIHAGGLNLEPF-----LKR 54
DB 177 ELEIDASLQSY-----EPKSLKIQNVSHLHKMKHLLLEIFVDLTSSVECLELR 230
QY 55 DADADPROVAD---TVKALRVERLTWGAAQVPAQLLVGLARVLA-YSLKELTLDLKI 109
DB 231 DTDLDTFHSELSGTGNSL-INKFTFRNVKTTDESLFQVMKLSQISGLELEFDDCTL 289
QY 110 TGTMPPLPLEATGLALLSLRLNRVSWATGRSMIAELQWLKPG-LKVLSTIAQHSFAF-- 166
DB 290 NG-----VDFRGSDDNDVIDPGKVETVIRRLHIHQFYS 324
QY 167 -----SYEQVRAF--PALTS-----LQSDNPGLGGERGLMAALCP 199
DB 325 FNDLSTLYPLTRVRKVTIVNSKFLVPCLLSRHLKSLBYLDLSENL-MVEEYLNKNSACE 383
QY 200 HKFPAIQNLALRNTGEMTPTGVCALAAAG-----VQPHSLDLSHSLRATVNPSPAPRC 253
DB 384 DAWPSIQTLILRQNL-----ASLGKGTGELLTKNLTNLDISKV-----TFHYMPETC 432

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QY 254 MWSSALNSINLSFAGLEQVPKCLPAKLVLDLSCNLRNAPQDPDELPEVDNLTLDGNPFL 313
DB 433 QMPEKKNYLSNSTRIHSVTGCIPTKLTLEILDISNNLNLFSL--NLPOLKELYISRNKIM 490
QY 314 VPGTALPHEGSMNSGVWPACARSTLS 339
DB 491 ---TLPDASLLPMLLVLKISNTIT 512

RESULT 9
TLR1 HUMAN
ID TLR1 HUMAN STANDARD; PRT; 786 AA.
AC Q15399; O15452; Q9UG90.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like) (TIL).
GN TLR1 OR KIAA0012.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN RN SEQUENCE FROM N.A.
RP TISSUE=Erythrocytes;
RC MEDLINE=9611856; PubMed=9435236;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila Toll.";
RN RN [2]
RP Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RP SEQUENCE FROM N.A.
RP TISSUE=Bone marrow;
RC MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RN RN [3]
RP DNA Res. 1:27-35(1994).
RN RN [4]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.-W., Otenwaelder B., Obermaier B., Poustka A.;
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RN RN [4]
RP Genome Res. 11:422-435(2001).
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
RX MEDLINE=20531768; PubMed=11081518;
RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domains.";
RN RN [4]
RP Nature 408:111-115(2000).
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (By similarity).
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.

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Db 370 F 370

RESULT 6

FLII DROME STANDARD; PRT; 1256 AA.

AC Q24020: Q24089; Q9VRH0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Flightless-I protein.

GN FLII OR CGI484.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Oregon-R; TISSUE=Embryo;

RX MEDLINE=94068608; PubMed=8248259;

RA Campbell H.D., Schimansky T., Claudianos C., Oszarac N.,

RA Kasprzak A.B., Cotwell J.N., Young I.G., de Couet H.G., Miklos G.L.G.;

RT "The Drosophila melanogaster flightless-I gene involved in

RT gastrulation and muscle degeneration encodes gelsolin-like and

RT leucine-rich repeat domains and is conserved in Caenorhabditis elegans

and humans.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:11386-11390(1993).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT SER-601.

RC STRAIN=Canton-S;

RX MEDLINE=96129280; PubMed=8582612;

RA de Couet H.G., Fong K.S.K., Weeds A.G., McLaughlin P.J.,

RA Miklos G.L.G.;

RT "Molecular and mutational analysis of a gelsolin-family member encoded

RT by the flightless I gene of Drosophila melanogaster.";

RL Genetics 141:1049-1059(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S;

RX MEDLINE=98188272; PubMed=9520435;

RA Maleszka R., de Couet H.G., Miklos G.L.G.;

RT "Data transferability from model organisms to human beings: insights

RT from the functional genomics of the flightless region of Drosophila.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3731-3736(1998).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196012; PubMed=10731138;

RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Friese E.,

RA Stapleton M., Harvey D.A.;

RT "A Drosophila complementary DNA resource.";

RL Science 287:2222-2224(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunderson R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [6]

RP REVISIONS.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

CC -!- FUNCTION: May play a key role in embryonic cellularization by

interacting with both the cytoskeleton and other cellular

components. Alternatively, it may play a structural role in

indirect flight muscle. Vital for embryonic development.

CC -!- TISSUE SPECIFICITY: Found in ovaries, larval fat bodies, brain and

adult thorax.

CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.

CC -!- DOMAIN: CONSISTS OF A LEUCINE-RICH AMINO TERMINAL HALF, WHICH IS

LIKELY TO BE INVOLVED IN PROTEIN-PROTEIN INTERACTION, AND A

CARBOXYTERMINAL HALF WHICH HAS HIGH SEQUENCE SIMILARITY TO

GELSOLIN AND IS THEREFORE LIKELY TO BE INVOLVED IN ACTIN-BINDING.

CC -!- SIMILARITY: Belongs to the villin/gelsolin family.

CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.

CC -!- SIMILARITY: Contains 4 gelsolin-like repeats.

CC -----

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CC -----

DR EMBL; U01182; AAC03566.1; -

DR EMBL; AF017777; AAC28407.1; -

DR EMBL; AF132184; AAD34772.1; -

DR EMBL; AE003568; AAF50830.2; -

DR F01; S60461; S60461.

DR HSP; P02640; 2VIL.

DR FlyBase; FBgn0000709; flil.

DR InterPro; IPR007122; Gelsolin.

DR InterPro; IPR007123; Gelsolin.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR003591; LRR_type.

DR Pfam; PF00626; Gelsolin; 5.

DR Pfam; PF00560; LRR; 12.

DR PRINTS; PR00597; GELSOLIN.

DR PRINTS; PR00019; LEURICHRPT.

RESULT 4	
CD14 MOUSE	
ID	CD14_MOUSE STANDARD; PRT; 366 AA.
AC	P10810;
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein).
DE	CD14.
GN	CD14.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
SEQUENCE FROM N.A.	
RP	STRAIN=BALB/c; TISSUE=Liver;
RC	STRAIN=ICR; TISSUE=Macrophage;
RK	MEDLINE=89183627; PubMed=2467257;
RA	Mayazaki Y., Setoguchi M., Yoshida S., Higuchi Y., Akizuki S., Yamamoto S.;
RA	"Nucleotide and amino acid sequences of the mouse CD14 gene.";
RT	Nucleic Acids Res. 17:2132-2132(1989).
RJ	[2]
SEQUENCE FROM N.A.	
RP	STRAIN=ICR; TISSUE=Macrophage;
RC	STRAIN=ICR; TISSUE=Macrophage;
RK	MEDLINE=89287330; PubMed=2472171;
RA	Setoguchi M., Nasu N., Yoshida S., Higuchi Y., Akizuki S., Yamamoto S.;
RA	"Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary structure deduced from cDNA clones.";
RT	Biochim. Biophys. Acta 1008:213-222(1989).
RJ	[3]
SEQUENCE FROM N.A.	
RP	MEDLINE=90293480; PubMed=1694207;
RA	Ferrero E., Hsten C.L., Francke U., Goyert S.M.;
RT	CD14 is a member of the family of leucine-rich proteins and is encoded by a gene syntenic with multiple receptor genes.";
RJ	J. Immunol. 145:331-336(1990).

RA	SEQUENCE FROM N.A.
RP	STRAIN=NMRI; TISSUE=Mammary gland;
RC	MEDLINE=2238857; PubMed=1247932;
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Scapleton M., Usdin T.B., Tohyuki S., Carinco P., Prange C.,
RA	Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Raha S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Richardson D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Valladao D.K., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Fahy J., Helton E., Kettelman M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Whiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
RA	Blakesley A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA	Rodriguez Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903(2002).
CC	-i- FUNCTION: Cooperates with MD-2 and TLR4 to mediate the innate
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via
CC	MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC	secretion and the inflammatory response. Up-regulates cell surface
CC	molecules, including adhesion molecules. (By similarity).
CC	-i- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC	multi-protein complex containing at least CD14, MD-2 and TLR4 (By
CC	similarity).
CC	-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC	-i- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collabor
CC	between the Swiss Institute of Bioinformatics and the EMBL outstat
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CC	entities requires a license agreement (See http://www.isb-sib.ch/anno
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X13987; CAA32166.1; -
DR	EMBL; X13333; CAA31710.1; -
DR	EMBL; M34510; AAA37387.1; -
DR	EMBL; BC057889; AAH57889.1; -
DR	PIR; S03605; TDMSW4.
DR	MGI; 88318; Cdl4.
DR	InterPro; IPR001611; LRR.
DR	Pfam; PF00560; LRR; 2
DR	PRINTS; PR00019; LEURICRPT.
KW	Immune response; Inflammatory response; Signal; GPI-anchor; Repeat;
KW	Leucine-rich repeat; Glycoprotein; Antigen; Lipoprotein.
FT	SIGNAL 1 15
FT	CHAIN 16 336 MONOCYTE DIFFERENTIATION ANTIGEN CD14.
FT	PROPEP 337 366 REMOVED IN MATURE FORM (POTENTIAL).
FT	REPEAT 79 105 LRR 1.
FT	REPEAT 111 135 LRR 2.
FT	REPEAT 189 215 LRR 3.
FT	REPEAT 217 239 LRR 4.
FT	REPEAT 244 267 LRR 5.
FT	REPEAT 269 292 LRR 6.
FT	REPEAT 294 314 LRR 7.
FT	CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID 336 336 GPI-anchor amidated asparagine
FT	(POTENTIAL).
SQ	SEQUENCE 366 AA; 39203 MW; 57C4492EC7EA3AA1 CRC64;

```
RT protein.";
RL J. Exp. Med. 175:1697-1705(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid;
RA Ishida T., Setoguchi M., Matsuura K., Yasunori H., Akizuki S.,
RA Yamamoto S.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cooperates with MD-2 and TLR4 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAF6 and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response. Up-regulates cell surface
CC molecules, including adhesion molecules (By similarity).
CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, MD-2 and TLR4 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
CC
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M85233; AAA31195.1; -.
CC EMBL; D16545; BAA21770.1; -.
CC InterPro; IPR001611; LRR.
CC Pfam; PF00560; LRR; 1.
CC
CC Immune response; Inflammatory response; Signal; GPI-anchor; Repeat;
CC Leucine-rich repeat; Glycoprotein; Antigen.
CC
CC SIGNAL 1 17
CC CHAIN 18 372 MONOCYTE DIFFERENTIATION ANTIGEN CD14.
CC REPEAT 194 220 LRR 1.
CC REPEAT 222 247 LRR 2.
CC REPEAT 249 271 LRR 3.
CC REPEAT 272 295 LRR 4.
CC REPEAT 297 315 LRR 5.
CC REPEAT 316 338 LRR 6.
CC CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 372 AA; 33992 MW; F9D6A997DD8825CC CRC64;
CC
CC Query Match 72.7%; Score 1338.5; DB 1; Length 372;
CC Best Local Similarity 73.5%; Pred. No. 3.5e-98;
CC Matches 261; Conservative 34; Mismatches 55; Indels 5; Gaps 2;
CC
CC QY 2 TPPECLDDEDFRCVNCNFPQDWSAEAFQCVSAVEVEIHAGLNLEPFLKRYVDADADR 61
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC 21 TPPECLDDEDFRCVNCNFPQDWSAEAFQCVSAVEVEIHAGLNLEPFLKRYVDADADR 80
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC
CC QY 62 QYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTM-PLPLEA 120
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 81 RYADVVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTM-PLPLEA 140
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC
CC QY 121 TGLALSRLRNVSWSATGRSLWLAELQWLKPKGLVLSIAQAHSAPFSYEQVRAFPALTSL 180
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 141 TGPLSTLSLRNVSWSATGRSLWLAELQWLKPKGLVLSIAQAHSAPFSYEQVRAFPALTSL 200
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC
CC QY 181 DLSDNPGGLGRGLMAALCPHKFFPAIONIALRNNTGMEPTGVCALAAAGVQPHSLDLSHN 240
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 201 DLSENFGGLGRGLVVAALCPHKFFPAIONIALRNNTGMEPTGVCALAAAGVQPHSLDLSHN 260
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC
CC QY 241 SLBATVNSAPRCMWSALNSLNSFAGLEQVQPKGLPAKLRLVLDLSNRLNRAAPQDELP 300
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 261 SLRA----DTQRCIWPSSALNSLNSFTGLQVQPKGLPAKLRLVLDLSNRLNRAAPQDELP 316
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC
CC QY 301 EVDNLTLDGNPFLVPGASKLQEDLTNSGVFPACPPSLAMGSGTLALQGARGP 355
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 317 KVNVLSDGNPFLVPGASKLQEDLTNSGVFPACPPSLAMGSGTLALQGARGP 371
Db
RESULT 3
CD14_BOVIN
ID CD14_BOVIN STANDARD; PRT; 373 AA.
AC Q95122; Q9TVA7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific
DE leucine-rich glycoprotein).
GN CD14.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RC MEDLINE=97445486; PubMed=9300371;
RA Ikeda A., Takata M., Taniguchi T., Sekikawa K.;
RT "Molecular cloning of bovine CD14 gene.";
RL J. Vet. Med. Sci. 59:715-719(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein-Friesian;
RA Filipp D., Julius M.J.;
RT "Cloning of cDNA for bovine CD14.";
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OP 179-278 FROM N.A.
RX MEDLINE=96209874; PubMed=8643545;
RA Diamond G., Russell J.P., Bevins C.L.;
RT "Inducible expression of an antibiotic peptide gene in
RT lipopolysaccharide-challenged tracheal epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5156-5160(1996).
CC -!- FUNCTION: Cooperates with MD-2 and TLR4 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAF6 and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response. Up-regulates cell surface
CC molecules, including adhesion molecules (By similarity).
CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, MD-2 and TLR4 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D84509; BAA21517.1; -.
CC EMBL; AF141313; AAD32215.1; -.
CC DR EMBL; U48356; AAB07861.1; -.
CC InterPro; IPR001611; LRR.
CC Pfam; PF00560; LRR; 2.
CC
CC Immune response; Inflammatory response; Signal; GPI-anchor; Repeat;
CC Leucine-rich repeat; Glycoprotein; Antigen.
CC SIGNAL 1 20
CC CHAIN 21 373 MONOCYTE DIFFERENTIATION ANTIGEN CD14.
CC REPEAT 192 218 LRR 1.
CC REPEAT 220 242 LRR 2.
CC REPEAT 245 270 LRR 3.
CC REPEAT 273 296 LRR 4.
CC REPEAT 298 316 LRR 5.
CC REPEAT 317 337 LRR 6.
```

FT	SIGNAL	1	19	CD14 DIFFERENTIATION ANTIGEN.
FT	CHAIN	20	375	CD14 DIFFERENTIATION ANTIGEN, URINARY
FT	CHAIN	20	367	FORM.
FT	CHAIN	20	345	MONOCYTE DIFFERENTIATION ANTIGEN CD14.
FT	PROPEP	346	375	REMOVED IN MATURE FORM (POTENTIAL).
FT	REPEAT	115	139	LRR 1.
FT	REPEAT	193	219	LRR 2.
FT	REPEAT	221	243	LRR 3.
FT	REPEAT	246	272	LRR 4.
FT	REPEAT	275	296	LRR 5.
FT	REPEAT	297	320	LRR 6.
FT	REPEAT	322	340	LRR 7.
FT	CARBOHYD	37	37	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	282	282	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	323	323	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	345	345	GPI-anchor amidated asparagine (Potential).
FT	CONFLICT	77	77	A -> G (IN REF. 3).
FT	CONFLICT	187	187	C -> Y (IN REF. 1 AND 2).
FT	CONFLICT	303	303	D -> E (IN REF. 5).
FT	SEQUENCE	375 AA;	40076 MW;	1746CDB41F394F8D CRC64;
SQL				
	Query Match		99.5%;	Score 1831; DB 1; Length 375;
	Best Local Similarity		99.7%;	Pred. No. 5.5e-137;
	Matches 355;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1	TTPEPELDEDEDPRVCNFPSEPODWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADADP	60	
DB	20	TTPEPELDEDEDPRVCNFPSEPODWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADADP	79	
QY	61	ROYADTVKALRVRLITVGAQVPAQLLVGALRVLAYSRRLKELTLEDLKITGTMPPLEA	120	
DB	80	ROYADTVKALRVRLITVGAQVPAQLLVGALRVLAYSRRLKELTLEDLKITGTMPPLEA	139	
QY	121	TGLALSSRLRNVSWATGRSWLAELQOWLKPGLKVLISIAQAHSPAFSVQVRAFPALTS	180	
DB	140	TGLALSSRLRNVSWATGRSWLAELQOWLKPGLKVLISIAQAHSPAFSVQVRAFPALTS	199	
QY	181	DLSDNPGLGERGLMAALCPHKFFPAIQNALRNTGMETPTGVCALAALAAAGVQPHSLDLSHN	240	
DB	200	DLSDNPGLGERGLMAALCPHKFFPAIQNALRNTGMETPTGVCALAALAAAGVQPHSLDLSHN	259	
QY	241	SLRATVNPSAPRCWSSALNSLNSPAGLQVQPKGLPAKRVLDLSCNRLNRAPOPDDEL	300	
DB	260	SLRATVNPSAPRCWSSALNSLNSPAGLQVQPKGLPAKRVLDLSCNRLNRAPOPDDEL	319	
QY	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVCGVSGTLLVQARGFA	356	
DB	320	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVCGVSGTLLVQARGFA	375	
	RESULT 2			
	CD14 RABIT	STANDARD;	PRT;	372 AA.
ID	CD14 RABIT			
AC	Q28680;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific			
DE	leucine-rich glycoprotein).			
GN	CD14.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92268819; PubMed=1375269;			
RA	Lee J.D., Kato K., Tobias P.S., Kirkland T.N., Ulevitch R.J.;			
RT	"Transfection of CD14 into 702/3 cells dramatically enhances the			
RT	sensitivity to complexes of lipopolysaccharide (LPS) and LPS binding			

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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 25 Seconds
(without alignments)
741.479 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPPCELDDDFRCVCFNS.....TLGVSGTIVLLQGARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1831	99.5	375	1	CD14 HUMAN
2	1338.5	72.7	372	1	CD14_RABIT
3	1328.5	72.2	373	1	CD14_BOVIN
4	1136.5	61.8	366	1	CD14_MOUSE
5	1079	58.6	371	1	CD14_RAT
6	150.5	8.2	1256	1	FLII DROME
7	147.5	8.0	784	1	TLR2_HUMAN
8	144	7.8	784	1	TLR2_MACFA
9	144	7.8	786	1	TLR1_HUMAN
10	142	7.7	1192	1	EXS ARATH
11	138	7.5	795	1	TLR1_MOUSE
12	138	7.5	1021	1	PSKR DAUCA
13	135	7.3	781	1	TL22_CHICK
14	130.5	7.1	784	1	TLR2_CRIGR
15	130.5	7.1	784	1	TLR2_MOUSE
16	129.5	7.0	784	1	TLR2_BOVIN
17	126.5	6.9	1196	1	BR11 ARATH
18	124	6.7	662	1	GARP HUMAN
19	122.5	6.7	605	1	ALS PAFPA
20	120.5	6.5	1008	1	PSKR ARATH
21	120	6.5	793	1	TL21_CHICK
22	118.5	6.4	796	1	TLR6_HUMAN
23	118.5	6.4	811	1	TLR4_HUMAN
24	117	6.4	327	1	OPT CANFA
25	113.5	6.2	1024	1	POPC RALSO
26	113	6.1	481	1	NYX HUMAN
27	112.5	6.1	1032	1	TLR9_HUMAN
28	112.5	6.1	1032	1	TLR9_MOUSE
29	112	6.1	858	1	TLR5_HUMAN
30	112	6.1	1115	1	TBC2_CHLRE
31	111	6.0	828	1	LGR6_HUMAN
32	111	6.0	899	1	ZCH2_HUMAN
33	110	6.0	574	1	IPA4_SHIFL

ALIGNMENTS

RESULT 1
CD14 HUMAN
ID CD14_HUMAN STANDARD; Q96L99; Q9UN33; PRT; 375 AA.
AC P08571; Q96FR6; Q96L99; Q9UN33;
DT 01-AUG-1988 (Rel. 08, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein).
DE leucine-rich glycoprotein.
GN CD14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=88234022; PubMed=2453848;
RA Ferrero E., Goyert S.M.;
RT "Nucleotide sequence of the gene encoding the monocyte differentiation antigen, CD14";
RL Nucleic Acids Res. 16:4173-4173 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258060; PubMed=3385210;
RA Haziot A., Chen S., Ferrero E., Low M.G., Silber R., Goyert S.M.;
RT "The monocyte differentiation antigen, CD14, is anchored to the cell membrane by a phosphatidylinositol linkage";
RL J. Immunol. 141:547-552 (1988).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Macrophage;
RX MEDLINE=89287330; PubMed=2472171;
RA Setoguchi M., Nasu N., Yoshida S., Higuchi Y., Akizuki S., Yamamoto S.;
RT "Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary structure deduced from cDNA clones";
RL Biochim. Biophys. Acta 1008:213-222 (1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89088540; PubMed=2462937;
RA Simmons D.L., Tan S., Tenen D.G., Nicholson-Weller A., Seed B.;
RT "Monocyte antigen CD14 is a phospholipid anchored membrane protein";
RL Blood 73:284-289 (1989).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Promyelocytic leukemia;
RA Long J.Y., Xue Y.N., Sun L., Wang H.X.;
RT "Cloning and sequencing of human CD14 gene";
RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:377-378 (1998).
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

34 109 5.9 605 1 ALS_HUMAN P35858 homo sapien
35 107.5 5.8 361 1 CHAD_BOVIN Q27972 bos taurus
36 107.5 5.8 1061 1 NA12_HUMAN P59046 homo sapien
37 107 5.8 1269 1 FLIH_HUMAN Q13045 homo sapien
38 106.5 5.8 331 1 PLIB_AGBEL O93233 agkistrodon
39 105.5 5.7 358 1 CHAD_RAT O70210 rattus norv
40 105.5 5.7 942 1 TMK1_ARATH P43298 arabidopsis
41 105.5 5.7 1504 1 SLIT_DROME P24014 drosophila
42 105 5.7 999 1 RLKS_ARATH P47735 arabidopsis
43 105 5.7 2224 1 FAS_HUMAN P12259 homo sapien
44 104.5 5.7 1315 1 CHAO_DROME P12024 drosophila
45 104 5.7 782 1 CHAO_TRICA P82963 tribolium c

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Db 105 YLQTLDSGNYFSGPLPDSLSNLTRLTLTVSGNSFSGSIPDS--VGMTV-----LEEL 157
QY 103 TLBDLKITGMPPLPLEATGLALSSLR-----LRNVSWATGRSWLAELQWLKPGGLKVL 157
Db 158 VLDSNRLYGSI-----ASNGLSLRLRLIQLNNIS-----189
QY 158 IQAHSFAFYEQVRAFPALTS-----LDLSDNPGLGERGLMAALCPHKFP-AIQNAL 210
Db 190 -----GEPDLSLKNLYLDASDN-----RISGRIPSELPESIVQISM 228
QY 211 RNTGMEPTGVCALAAAGVQPHS-----LDLSHNSLRATVNSAPRCMWS--SALN 260
Db 229 RNNLFQ-----GTPESFKLLNSLEVIDLSHNKLSGSI-----PSFIFTHQSLO 272
QY 261 SLNLSFAGLRQV-----PKGLPAKLRVLDLSCNR--LNRAPQDEL--PEVDNLTDGNPF 312
Db 273 QLTLSEFNGFTSLSEPYSPGLPSGLISVDLSNNQILGALPLFMGLSPKLSALSLENNKF 332
QY 313 -----LVPGT-----ALPHEGSMNSGVVP-----ACARSTLSVGVSG-----344
Db 333 FGMIPTQYVWKTSPGSEFAGFORLLGGNPLFGVFPGLMALKPGSANVOLAGNCFSWC 392
QY 345 --TIVLLQG 351
Db 393 PATLFFCQG 401
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RESULT 15

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Q8NI00 PRELIMINARY; PRT; 586 AA.
AC Q8NI00;
BT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Toll-like receptor 2 (Fragment).
Q8 Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Yu W.B., Ma Y.Y.;
RT "Cloning and sequencing of extracellular domain and its N-terminal and
RT C-terminal fragments of Toll-like receptor 2.";
RL T1 4 Chun i Ta Hsueh Heueh Pao 23:0-0(2002).
DR EMBL; AF502291; AAM23001.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 3.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Receptor.
FT NON TER.
SQ SEQUENCE 586 AA; 66281 MW; 6D676D752BE55C88 CRC64;
```

Query Match 8.0%; Score 147.5; DB 4; Length 586;

Best Local Similarity 22.3%; Pred. No. 0.0017;

Matches 82; Conservative 56; Mismatches 131; Indels 99; Gaps 17;

QY 4 EPCLEDDDEFCVCFSEFPQDWSEAFQCVSAVEIHHAGGLNLEPF-----LKR 54

Db 177 EELEIDASLQSY-----EPKSLKSTQNVSHLILHMKQHILLLEIFVDVTSSVECLELR 230

QY 55 DADADPRQYAD-----TVKALFRVRLTVGAQVPAQLLVGALRVL--AYSRLKELTLEDLKI 109

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Db 231 DTDLDTFHFSELSTGETNSL--IKKFTFRNVKITDESLSFQVMKLNQISGLLELEFFDDCTL 289
QY 110 TGTMPPLPLEATGLALSSLRNVSWATGRSWLAELQWLKPG--LKVLSTIAQAHSAPF-- 166
Db 290 NG-----VGNFRASDNRVIDPGKVETLTTRRLHIPRYL 324
QY 167 -----SYEQVRAF--PALTS-----LDLSDNPGLGERGLMAALCP 199
Db 325 FYDLSTLYSLTERVKRITVENSKVFIIVPCLLSQHLKSLEYLDLSEN--MVVEYLKNSACE 383
QY 200 HKFPAIQNALRNTGMEPTGVCALAAAG-----VOPHSLDLSHNSLRATVNSAPR-- 252
Db 384 DAMFSLQTLILRQNL-----ASLEKTGETLTILKNTLNIDISKNSFH-----SMPET 431
QY 253 CMWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELPEVDNLTDGNPF 312
Db 432 COMPEKMYLNSSTRISHSVTGCIPKTKLEILDVSNNNLNFSL--NLPQKELYISRNKL 489
QY 313 L-VPGTAL 319
Db 490 MTLPDASL 497
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Search completed: October 4, 2004, 16:51:23

Job time : 124 secs

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ID Q865B9 PRELIMINARY; PRT; 1079 AA.
AC Q865B9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Toll-like receptor 9 protein.
GN TLR9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Hasimoto M.;
RT "Molecular cloning of canine TLR9 gene.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Hashimoto M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB1304899; BAC65192.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; WHHArAc.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR001266; Ribosomal_S19E.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 12.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD003854; Ribosomal_S19E; 1.
DR SMART; SM00364; LRR_BAC; 4.
DR SMART; SM00366; LRR_PS; 10.
DR SMART; SM00365; LRR_SD22; 4.
DR SMART; SM00369; LRR_TYP; 16.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS0104; TIR; 1.
KW Receptor.
SQ SEQUENCE 1079 AA; 120349 MW; CA95D91D12D33C8E CRC64;

Query Match 8.1%; Score 148.5; DB 6; Length 1079;
Best Local Similarity 28.3%; Pred. No. 0.0032;
Matches 90; Conservative 48; Mismatches 113; Indels 67; Gaps 18;

Qy 71 RVRELTVGAQVPAQLVGALRVLAYSELKLTLEDLKITGMPLPLEATGLALSSRL 130
Db 335 RLRLRN-----LSFNHYHKVSPFAHLHLASSFGL-LSLQELDIHGIF 376
Qy 131 RNVSWATGRSWLAELQOOWLKPGIKVLSIAQAHSFAPSYEQVRAFPALTSLDLSDN--PGL 188
Db 377 RSLSETTLQS-LAHLPLMLRHLQINFTISOQLSIFG-----APFGLRYVLDLSDNRISGA 430
Qy 189 GE----RGLMAALCPHK-FPAIQNALRLNTGMETPTGVCAALAAAGVQPHSLDLSHNSLR 243
Db 431 AEPAAATGEVEADCGERWMPQSRDLAPLGL--TP-GSEAFMPSCRTLNFLLDLSRNL- 486
Qy 244 ATVNP-----SAPRCWSSALNSLNSIFAGLEQVPKGLPAKLRVLDLSCNRLN--RAPQ 295
Db 487 VTVOPEMFVRLARLQCLGLSH-NSISQAVNGSQFVPL---SNLRVLDLSHNKLDTYHGRS 542
Qy 296 PDELPEVDNLTLDCN--PFLVPGT-----ALPHEGSMNSGVVPACARST 337
Db 543 FTELPRLEALDLSYNSQFPMRGVCHNLFSVAQLPAURLYLSLAHNG-IHSRVSOOLRSAS 601
Qy 338 L-SVGVSGTLLVLLQARG 354

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[illegible]

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Query Match      8.0%; Score 148; DB 10; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.00098;
Matches 104; Conservative 55; Mismatches 106; Indels 164; Gaps 26;

Qy 4 EPELDDDD-----FRC-----VCNFESEQPDWSEAFQCVCVSAVEEIHAGGLKLEP 49
   ||| |||
Db 56 DPCDNIFSDFTFCGRCDSSVVTGSGRVTELSLDQAGYSGSLSSVS-----FNL-P 104

Qv 50 FLKRVDADAD--PROVADTVKAL-RVRRIRIVG-----AAQVPAOLLVGLRIVLAYSRIKEL 102

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Db 1 IRGGHSLDQPKGV--NTDPKQYADTIKALVRRLKGAQAQVPAQLLVAVLRALGYSL 58
Qy 100 KETLEDLKLTGTWPPPLPLEATGALSLRLRNYSWATGRSWLAELQWLKPLKVLISIA 159
Db 59 KETLEDLEVTGTPPTPLEATGPALTTLRLNYSWATGGAWLGELOQWLKPLKRLNIA 118
Qy 160 QAHSFATSYEQVRAFPALTSLDLSDNPGLGERGLMAALCP 199
Db 119 QAHSFATPACGLSTFEALTTLSDNPSLSDSGLMAALCP 158

RESULT 10
Q8HY29 PRELIMINARY; PRT; 106 AA.
AC Q8HY29
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lipopolysaccharide receptor (Fragment).
GN CD14.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Blood;
RA Prgomet C., Sarikaya H., Bruckmaier R.M., Pfaffl M.W.;
RT "Isolation and characterization of leukocyte subpopulations in ovine
RT blood and milk."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535322; CAD59477.1; -.
GO GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 1.
KW Receptor.
FT NON TER 1
FT NON TER 106
FT NON TER 106
SQ SEQUENCE 106 AA; 10973 MW; 4EEB025D18A96D8 CRC64;

Query Match 23.5%; Score 431.5; DB 6; Length 106;
Best Local Similarity 80.4%; Pred. No. 1.1e-27;
Matches 86; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 179 SLDSDNPGLGERGLMAALCPKPAQNLALRNTGMEPTGVCALAAAGVQPHSLDLS 238
Db 1 TLDSDNPSLSDSGLMAALCPKFPALQYLALRNTGMEPTGVCALAAAGVQPHSLDLS 60
Qy 239 HNSLRATVNSAPRCMSSALNSLNSLSPAGLEQVQPKGLPAKLRLVLDL 285
Db 61 HNSLRVTA-PGATRCVWPSALSSUNLSLSPAGLEQVQPKGLTKLSVLDL 106

RESULT 11
Q88955 PRELIMINARY; PRT; 128 AA.
AC Q88955
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monocyte differentiation antigen CD14 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; TISSU=Testis;
RX MEDLINE=20314485; PubMed=10854787;
RA Liu S., Shapiro R.A., Nie S., Zhu D., Vodovotz Y., Billiar T.R.;
RT "Characterization of rat CD14 promoter and its regulation by
RT transcription factors Ap1 and Sp family proteins in hepatocytes."

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RL Gene 250:137-147(2000).
DR EMBL; AF087944; AAC35372.1; -.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14265 MW; 012C8DB034580234 CRC64;

Query Match 17.7%; Score 326; DB 11; Length 128;
Best Local Similarity 57.9%; Pred. No. 5.8e-19;
Matches 62; Conservative 18; Mismatches 25; Indels 2; Gaps 1;

Qy 2 TPEPCEL--DDEDFRCVNFSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAAD 59
Db 21 TPEPCELDDQDESVRCYCNFSDPOPWNSSAFCAEDVEFYGGRSLEYLLKRVDTAN 80
Qy 60 PROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLED 106
Db 81 LGQYTDIIRSLPLKRLTVRSARVPTQLFLGLRVLYSGSLRELTLLEN 127

RESULT 12
Q940E8 PRELIMINARY; PRT; 613 AA.
ID Q940E8
AC Q940E8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fasciated ear2.
GN FE2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21521230; PubMed=11641280;
RA Taguchi-Shiobara F., Yuan Z., Hake S., Jackson D.;
RT "The fasciated ear2 gene encodes a leucine-rich repeat receptor-like
RT protein that regulates shoot meristem proliferation in maize."
RL Genes Dev. 15:2755-2766(2001).
DR EMBL; AY055124; AALI7871.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 13.
DR PRINTS; PR00019; LEURICHRPT.
SQ SEQUENCE 613 AA; 63951 MW; 554A8A76C878A977 CRC64;

Query Match 8.2%; Score 151; DB 10; Length 613;
Best Local Similarity 27.9%; Pred. No. 0.00094;
Matches 81; Conservative 26; Mismatches 75; Indels 108; Gaps 15;

Qy 79 AAQVPAQLLVGALRVLAYSLKELTLEDLKLTGTMPPLPLEATGLALSSLR--LRNVSWA 136
Db 4 ATPLPHQLLATFLVLVA-----SATOPAVPASTDRAALLAFRASLSPPSRA 49
Qy 137 TGRSWLAELQ-QWLKPGKLVLSIAQAHSFATSYEQVRAFPALTSLDLSNPGLGERGLMA 195
Db 50 ALSWSGFLSPSWLG-----VSLHPATAPA-----PSVTT----- 79
Qy 196 ALCPHKFPAIQNLALRNTGMEPTGV-----CAALAAAGVQPHS----- 234
Db 80 -----PSVAELSLRGINL---TGVTPAAPALLRLRLTLDLSANALSGELPCSLPRSL 129
Qy 235 --LDLSHNSLRATVNSAPRCMSS--ALNSLNS--FAGLEQVQPK-GLPAKLRLVLDLSC 287
Db 130 LALDSRLNLSGAV-----PTCLPSSLPALRTNLNSANFLRLPLSPRLSFPARLALDLNR 185
Qy 288 NLRNRAFQPDDELPEVDN-----LTIDGNPFLLVPGTALPHEGSMNSGVVPA 332
Db 186 NAISGAVPRIVADPDNSALLLDDLSHNR-----SGEIPA 221

RESULT 13
Q865B9

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RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039060; BAB68584.1; -
DR EMBL; AB039062; BAB68586.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38081 MW; 8FF604FDB09631AD CRC64;

Query Match 61.7%; Score 1135.5; DB 11; Length 356;
Best Local Similarity 65.7%; Pred. No. 1.9e-84;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62
Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDLKITGTWPPPLEATG 122
Db 68 FTDIISLSKRLTVRAARIIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSEYQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDRAWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLAALRNAGMETPSCVCSALAAARVQLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKIPAKLRVLDLSCNRLNRAPODELPEV 302
Db 248 RDA--GAPSCDWPFSQLSNLSLFTGLKQVPGKIPAKLSVLDLSYNRLDRNPSDELPEV 305
Qy 303 DNLTLGDNPFVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQARGF 355
Db 306 GNLSIKGNPFL--DSRSHSEKYNSSGVVTAGAPSSQVALLSGTLALLLGDRLF 355

RESULT 5
Q91VC2 PRELIMINARY; PRT; 356 AA.
ID Q91VC2
AC Q91VC2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CAST/Ei, and HMI/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039061; BAB68585.1; -
DR EMBL; AB039062; BAB68586.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38100 MW; 28387B3A498506D2 CRC64;

Query Match 61.7%; Score 1135.5; DB 11; Length 356;
Best Local Similarity 65.7%; Pred. No. 1.9e-84;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62

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Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDLKITGTWPPPLEATG 122
Db 68 FTDIISLSKRLTVRAARIIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSEYQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDRAWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLAALRNAGMETPSCVCSALAAARVQLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKIPAKLRVLDLSCNRLNRAPODELPEV 302
Db 248 RDA--GAPSCDWPFSQLSNLSLFTGLKQVPGKIPAKLSVLDLSYNRLDRNPSDELPEV 305
Qy 303 DNLTLGDNPFVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQARGF 355
Db 306 GNLSIKGNPFL--DSRSHSEKYNSSGVVTAGAPSSQVALLSGTLALLLGDRLF 355

RESULT 6
Q920X6 PRELIMINARY; PRT; 356 AA.
ID Q920X6
AC Q920X6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ZEN;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039063; BAB68587.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38095 MW; 11041813429631B8 CRC64;

Query Match 61.5%; Score 1132.5; DB 11; Length 356;
Best Local Similarity 65.4%; Pred. No. 3.3e-84;
Matches 231; Conservative 41; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62
Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDLKITGTWPPPLEATG 122
Db 68 FTDIISLSKRLTVRAARIIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSEYQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDRAWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLAALRNAGMETPSCVCSALAAARVQLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKIPAKLRVLDLSCNRLNRAPODELPEV 302

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Db 138 GPPLSSRLRNVSATGAWLAEQWLKPGILKILSIAQHSLSAQSALHTLD 197
QY 182 LSDNPGGLGRLMAALCPHKFPAIQNALRNVTGTPGVCALAAAGVQPHSLDLSHNS 241
Db 198 LSDNPGGLGRLIAALCPHKFPALRLDARNAGMTGVCMAAAAGVQPHSLDLSHNS 257
QY 242 LRATVNSAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 301
Db 258 LSAAA-PGAPRCDFPALSLSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 316
QY 302 VDNLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTILVLLQGARGFA 356
Db 317 VSNLILDRNPFYLDPEAS--KQDQNSGVVAACAHSAHSALTIGSTLALLRGAGDFA 369

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RESULT 2

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Q920X8
ID Q920X8 PRELIMINARY; PRT; 356 AA.
AC Q920X8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BLG/Msf;
EA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
LR EMBL; AB039056; BAB68580.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER
SQ SEQUENCE 356 AA; 38169 MW; 8633BB9B2345D7A2 CRC64;

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```

Query Match 62.0%; Score 1140.5; DB 11; Length 356;
Best Local Similarity 66.0%; Pred. No. 7.4e-85;
Matches 233; Conservative 40; Mismatches 73; Indels 7; Gaps 3;

QY 3 PEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEVEIHAGLNLEPFLKRVADADPRQ 62
Db 10 PEPCELDEE--RCSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
QY 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYASRLKELTLEDLKITGTPPLPLEATG 122
Db 68 FTDIISLSLKLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
QY 123 LALSRLRNVSATGRSWLAELQWLKPLKVLISIAQHSLSAQSALHTLDLSNRLNRAPOQDELPE 182
Db 128 PDNLILNRNVSATGRSWLAELQWLKPLKVLISIAQHSLSAQSALHTLDLSNRLNRAPOQDELPE 187
QY 183 SDNPGGLGRLMAALCPHKFPAIQNALRNVTGTPGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPGGLGRLISALCPKLPFTLQVLARNAGMETPSPGVCALAAARVQLQGLDLSHNSL 247
QY 243 RATVNSAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 302
Db 248 RDA--GAPSCDWPQLNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 305
QY 303 DNLTLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTILVLLQGARGF 355
Db 306 GNLSLKGPNFL--DSESHSEKYNKSVVVTAGAPSSQVALSGTLLIGDLRF 355

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RESULT 3

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Q91VD3
ID Q91VD3 PRELIMINARY; PRT; 356 AA.
AC Q91VD3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWN/Msf, and NUL/Msf;
EA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
LR EMBL; AB039059; BAB68583.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER
SQ SEQUENCE 356 AA; 38065 MW; 17CD94FDB09631B3 CRC64;

```

```

Q91VD3
ID Q91VD3 PRELIMINARY; PRT; 356 AA.
AC Q91VD3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10SnJ, and pgn2;
EA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
LR EMBL; AB039054; BAB68578.1; -.
DR EMBL; AB039059; BAB68583.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER
SQ SEQUENCE 356 AA; 38065 MW; 17CD94FDB09631B3 CRC64;

Query Match 61.8%; Score 1136.5; DB 11; Length 356;
Best Local Similarity 65.7%; Pred. No. 1.6e-84;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

QY 3 PEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEVEIHAGLNLEPFLKRVADADPRQ 62
Db 10 PEPCELDEE--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
QY 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYASRLKELTLEDLKITGTPPLPLEATG 122
Db 68 FTDIISLSLKLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
QY 123 LALSRLRNVSATGRSWLAELQWLKPLKVLISIAQHSLSAQSALHTLDLSNRLNRAPOQDELPE 182
Db 128 PDNLILNRNVSATGRSWLAELQWLKPLKVLISIAQHSLSAQSALHTLDLSNRLNRAPOQDELPE 187
QY 183 SDNPGGLGRLMAALCPHKFPAIQNALRNVTGTPGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPGGLGRLISALCPKLPFTLQVLARNAGMETPSPGVCALAAARVQLQGLDLSHNSL 247
QY 243 RATVNSAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 302
Db 248 RDA--GAPSCDWPQLNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 305
QY 303 DNLTLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTILVLLQGARGF 355
Db 306 GNLSLKGPNFL--DSESHSEKYNKSVVVTAGAPSSQVALSGTLLIGDLRF 355

RESULT 4
Q91V69
ID Q91V69 PRELIMINARY; PRT; 356 AA.
AC Q91V69;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWN/Msf, and NUL/Msf;
EA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
LR EMBL; AB039055; BAB68580.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER
SQ SEQUENCE 356 AA; 38169 MW; 8633BB9B2345D7A2 CRC64;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 117 Seconds
(without alignments)
960.038 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTEPCLELDEDFRCVNFPS.....TLSSGVSGTLVLQARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp archea:*

2: sp bacteria:*

3: sp fungi:*

4: sp human:*

5: sp invertebrate:*

6: sp mammal:*

7: sp mhc:*

8: sp organelle:*

9: sp phage:*

10: sp plant:*

11: sp rodent:*

12: sp virus:*

13: sp vertebrate:*

14: sp unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1338.5	72.7	369	6 Q9TTT3	Q9ttt3 equus caball
2	1140.5	62.0	356	11 Q920X8	Q920x8 mus musculu
3	1136.5	61.8	356	11 Q91VD3	Q91vd3 mus musculu
4	1135.5	61.7	356	11 Q91V69	Q91v69 mus musculu
5	1135.5	61.7	356	11 Q91VC2	Q91vc2 mus musculu
6	1132.5	61.5	356	11 Q920X6	Q920x6 mus spicile
7	1131.5	61.5	356	11 Q920X9	Q920x9 mus musculu
8	1102	59.9	353	11 Q920X7	Q920x7 mus musculu
9	562	30.5	158	6 Q7YSB4	Q7yse4 ovis aries
10	431.5	23.5	106	6 Q8HY29	Q8hy29 ovis aries
11	326	17.7	128	11 Q88955	Q88955 rattus norv
12	151	8.2	613	10 Q940E8	Q940e8 zea mays [m
13	148.5	8.1	1079	6 Q865B9	Q865b9 canis famil
14	148	8.0	418	10 Q9FH56	Q9fh56 arabidopsis
15	147.5	8.0	586	4 Q8NI00	Q8ni00 homo sapien
16	144.5	7.9	353	4 Q9UJX9	Q9ujx9 homo sapien

17 144.5 7.9 353 4 Q8WUA8
18 144 7.8 1535 5 Q9VPR0
19 140.5 7.6 1178 10 Q942T3
20 140.5 7.6 1274 10 Q8LI55
21 140 7.6 1121 10 Q942F3
22 138 7.5 784 6 Q8MIQ3
23 137 7.4 1392 5 Q9VAD1
24 136.5 7.4 330 11 Q8K2A9
25 136.5 7.4 1007 10 Q9ZVD4
26 135 7.3 1096 10 Q8SD14
27 134.5 7.3 1030 10 Q8H037
28 133.5 7.3 833 10 Q852J5
29 132 7.2 605 16 Q8ZH98
30 131.5 7.1 784 11 Q811T5
31 130.5 7.1 1110 10 Q94LN2
32 130 7.1 290 2 Q8KNJ6
33 130 7.1 1024 16 Q8XS09
34 129 7.0 1143 10 Q9SUB9
35 128.5 7.0 342 11 Q91XL1
36 128.5 7.0 497 10 Q7XKC0
37 128.5 7.0 784 11 Q8K3D9
38 128.5 7.0 1013 10 Q8LQ10
39 128 7.0 291 16 Q8ZH99
40 128 7.0 444 4 Q9H5H8
41 128 7.0 453 4 Q86XY1
42 128 7.0 601 13 Q7SXW3
43 128 7.0 622 4 Q8N3E0
44 128 7.0 797 4 Q9UGS3
45 127.5 6.9 905 10 Q64757

ALIGNMENTS

RESULT 1

Q9TTT3 ID Q9TTT3 PRELIMINARY; PRT; 369 AA.
AC Q9TTT3;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Lipopolysaccharide receptor.
GN CD14.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandeplas M.L., Barton M.H., Tobias P.S., Moore J.N.;
RT "Cloning of the equine CD14 receptor and determination of its full-length cDNA sequence."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200416; AAF08963.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 1.
DR Receptor.
SQ SEQUENCE 369 AA; 39108 MW; F72B4168114A9ED3 CRC64;

Query Match 72.7%; Score 1338.5; DB 6; Length 369;
Best Local Similarity 74.6%; Pred. No. 5.3e-101;
Matches 265; Conservative 30; Mismatches 55; Indels 5; Gaps 3;
Qy 2 TPEPCLELDEDFRCVNFSPQDWSSAFQCVSAVEIHHAGLNLEFLKRVADADPR 61
Db 20 TLEPCEVDENFRVCNFTGPQDWSSAFQCVSAVEIHHAGLNLEFLKRVADADPR 77
Qy 62 QYADTVKALRVRLTVGAQVPAQLVGCALRVLAYSLKLTLELTKITGMPPLEBAT 121
Db 78 QYADIVKALRQRLTVGAVQVPAQLVALLRGLYSLKLTLELTKITGMPPLEBAT 137
Qy 122 GLALSRLRNVSQWATGSLAEIQWLKPLKVLSTIAQAHSPAFSYEQVRAFPALTSLD 181

Db 97 RQYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPLEA 156
Qy 121 TGLALSSLRRLNVSWATGRSWLAELQQLKPLKVLSTIAQAHSPAFSVEQVRAPALTSL 180
Db 157 TGLALSSLRRLNVSWATGRSWLAELQQLKPLKVLSTIAQAHSPAFSVEQVRAPALTSL 216
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIONLALNTGMETGTGCAALAAAGVQPHSLDLSHN 240
Db 217 DLSNPGGLGERGLMAALCPHKFPAIONLALNTGMETGTGCAALAAAGVQPHSLDLSHN 276
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPODPLP 300
Db 277 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPODPLP 336
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGAR 353
Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGAR 389

RESULT 15
AAR98576
ID AAR98576 standard; peptide; 348 AA.

XX AAR98576;
XX 07-FEB-1997 (first entry)

DE CD14 sequence.

XX Antinflammatory; lipopolysaccharide; LPS; Gram-positive bacteria; CD14;
KW treatment; septic shock; inflammatory bowel disease; liver failure;
KW graft versus host disease; pancreatitis; tuberculosis;
KW adult respiratory distress syndrome; detection; quantification.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Domain 1..56
FT /label= EGF-like domain
FT Disulfide-bond 6..15
FT Disulfide-bond 15..17
FT Disulfide-bond 17..32
FT Modified-site 18
FT /note= "Potential N-linked glycosylation site"
FT Region 57..64
FT /label= Linker
FT Region 65..283
FT /label= Core region
FT Disulfide-bond 168..198
FT Disulfide-bond 222..253
FT Modified-site 263
FT /note= "Potential N-linked glycosylation site"
FT Region 284..348
FT Disulfide-bond /label= Tail
FT Modified-site 287..333
FT /note= "Potential N-linked glycosylation site"

XX WO9620956-A1.

XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US016977.

XX 30-DEC-1994; 94US-00366953.

XX (AMGE-) AMGEN INC.
XX (UYRQ) UNIV ROCKEFELLER.

XX Lichenstein HS, Wright SD, Narhi LO, Juan S;

XX WPI; 1996-333943/33.

XX Peptide(s) based on CD14 sequences - which bind to lipo:poly:saccharide
PT and inhibit CD14 mediated inflammatory responses.
XX Disclosure; Fig 1; 103pp; English.
XX Antinflammatory peptides based on the human CD14 sequence (See AAR98570-
CC 75 and AAR98577-80) can bind to lipopolysaccharide (LPS) and inhibit
CC binding of LPS or Gram positive cell components to CD14, thus reducing or
CC eliminating CD14 mediated inflammatory responses. They can be used for
CC treating inflammatory conditions in particular, septic shock,
CC inflammatory bowel disease, acute and chronic liver failure, graft versus
CC host disease, intestinal or liver transplant, adult respiratory distress
CC syndrome, acute pancreatitis and tuberculosis. They can also be used to
CC remove, detect or quantitate LPS or Gram-positive cell components in
CC samples. The peptides are used in doses of 0.1-100 mg/kg by parenteral or
CC oral routes
XX
SQ Sequence 348 AA;

Query Match 97.3%; Score 1791; DB 2; Length 348;
Best Local Similarity 99.7%; Pred. No. 2.5e-164;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADAP 60
Db 1 TTPEPCELDDDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADAP 60
Qy 61 RQYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPLEA 120
Db 61 RQYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPLEA 120
Qy 121 TGLALSSLRRLNVSWATGRSWLAELQQLKPLKVLSTIAQAHSPAFSVEQVRAPALTSL 180
Db 121 TGLALSSLRRLNVSWATGRSWLAELQQLKPLKVLSTIAQAHSPAFSVEQVRAPALTSL 180
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIONLALNTGMETGTGCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHKFPAIONLALNTGMETGTGCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPODPLP 300
Db 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPODPLP 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLL 348

Search completed: October 4, 2004, 16:53:33
Job time : 130 secs

ID AAW41693 standard; protein; 375 AA.
XX AAW41693;
AC
XX 01-MAY-1998 (first entry)
XX Human CD14.
XX
XX Identification; binding inhibitor; lipopolysaccharide; LPS; CD14;
KW binding protein; LBP; monocyte receptor; treatment; septic shock; human.
XX
XX Homo sapiens.
OS
XX US5705398-A.
PN
XX 06-JAN-1998.
XX
XX 02-MAR-1994; 94US-00205719.
XX
XX 02-MAR-1994; 94US-00205719.
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX Tobias P, Mintz DN, Ulevitch R;
PI
XX WPI; 1998-086145/08.
DR N-PSDB; AAV05505.
DR
XX Assay for lipo:poly:saccharide binding inhibitors - useful in the
PT treatment of septic shock and other lipo:poly:saccharide-mediated
PT disorder(s).
XX
XX
PS Claim 9; Col 19-22; 21pp; English.
XX
XX The present sequence was used in the development of a novel method for
CC identifying a compound that inhibits the binding of a lipopolysaccharide
CC (LPS) to a LPS-binding protein (LBP), or LBP-dependent binding of LPS to
CC monocyte receptor CD14. The method comprises measuring the fluorescence
CC emitted by a reaction mixture containing fluoresceinated LPS, isolated
CC LBP and optionally CD14 in the presence and absence of the compound, and
CC identifying the compound as an inhibitor if the fluorescence emitted by
CC the reaction mixture containing the compound is less than that emitted by
CC the reaction mixture that does not contain the compound. The method can
CC be used to identify drugs useful for treating septic shock and related
CC LPS-mediated disorders
XX
SQ Sequence 375 AA;
Query Match 99.2%; Score 1826; DB 2; Length 375;
Best Local Similarity 99.4%; Pred. No. 1.1e-167; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 2;
QY 1 TTPEPCELDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP 60
DB 20 TTPEPCELDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP 79
QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDKITGTMPLEA 120
DB 80 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDKITGTMPLEA 139
QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPLGLKVLSTQAQHSFAPSVQVRAFPALTSL 180
DB 140 TGLALSSLRNVSWATGRSWLAELQWLKPLGLKVLSTQAQHSFAPSVQVRAFPALTSL 199
QY 181 DLSNPGGLGRLMAALCPHKFPAIONLALRNTGWTPTGVCAALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGRLMAALCPHKFPAIONLALRNTGWTPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSCNRLNRAPOPEL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSCNRLNRAPOPEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQARGFA 356

DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQARGFA 375
RESULT 14
AAB58147
ID AAB58147 standard; protein; 431 AA.
XX
AC AAB58147;
XX
DT 14-MAR-2001 (first entry)
XX
DE Lung cancer associated polypeptide sequence SEQ ID 485.
XX
KW Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX
OS Homo sapiens.
XX WO200055180-A2.
PN
XX 21-SEP-2000.
PD
XX 08-MAR-2000; 2000WO-US005918.
PF
XX 12-MAR-1999; 99US-0124270P.
PR
XX (HOMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Ruben SM;
PI
XX WPI; 2000-587514/55.
DR N-PSDB; AAF18023.
DR
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
XX
PS Claim 11; Page 967-968; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
SQ Sequence 431 AA;
Query Match 98.2%; Score 1807; DB 3; Length 431;
Best Local Similarity 99.2%; Pred. No. 9.6e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTPEPCELDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP 60
DB 37 TTPEPCELDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP 96
QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDKITGTMPLEA 120

PN WO2003057160-A2.
 XX 17-JUL-2003.
 PD 30-DEC-2002; 2002WO-US041798.
 PF 02-JAN-2002; 2002US-0345444P.
 XX 25-JAN-2002; 2002US-0351885P.
 PR 25-FEB-2002; 2002US-0360066P.
 PR 05-MAR-2002; 2002US-0362004P.
 PR 20-MAR-2002; 2002US-0368669P.
 PR 21-MAR-2002; 2002US-0366284P.
 PR 28-MAR-2002; 2002US-0368679P.
 PR 19-AUG-2002; 2002US-0404809P.
 PR 21-AUG-2002; 2002US-0405645P.
 XX (GETH) GENENTECH INC.

XX Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;
 PI Williams PM, Wu TD, Zhang Z;
 XX WPI; 2003-569537/53.
 DR N-PSDB; ADD89093.
 XX

PT New antibodies against tumor-associated antigenic target polypeptide,
 PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
 PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 PT carcinomas.

XX Claim 1; SEQ ID NO 23; 252pp; English.

XX The present invention relates to antibodies against tumour-associated
 CC antigenic target polypeptide. The antibody is useful for treating or
 CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung
 CC cancer, breast cancer, colon cancer, ovarian cancer, prostate
 CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The
 CC present sequence represents a TAT polypeptide.

XX Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 7; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDEDFRCVNFSEPOQDMSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 DB 20 TTPEPCELDDEDFRCVNFSEPOQDMSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLRKELTLEDLKITGTMPPPLEA 120
 DB 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLRKELTLEDLKITGTMPPPLEA 139
 QY 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPPALTSL 180
 DB 140 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPPALTSL 199
 QY 181 DLSNDPGLGERGLMAALCPHKFPFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
 DB 200 DLSNDPGLGERGLMAALCPHKFPFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRAFPQDELP 300
 DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRAFPQDELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 12
 ID AAO22313
 XX AAO22313 standard; protein; 356 AA.

AC AAO22313;
 XX 11-OCT-2002 (first entry)
 DT Anti-CD14 monoclonal antibody related protein SEQ ID No 1.
 DE Immunosuppressive; antibacterial; anti-CD14 antibody; epitope; sepsis;
 KW human CD14.
 XX Homo sapiens.
 OS WO200242333-A1.
 PN 30-MAY-2002.
 PD 28-SEP-2001; 2001WO-JP008563.
 PF 22-NOV-2000; 2000JP-00356719.
 PR (MOCH) MOCHIDA PHARM CO LTD.
 PA Furusako S, Shirakawa K, Mori S;
 XX WPI; 2002-454920/48.
 DR Anti-CD14 monoclonal antibody which inhibits CD14/T lymphocyte receptor
 PT binding by specifically recognizing epitope in human CD14 domain to
 PT prevent interaction and suppress cell activation, useful for treating
 PT sepsis.
 XX Claim 10; Page 109-112; 156pp; Japanese.
 PS The invention relates to an anti-CD14 antibody which can specifically
 CC recognise an epitope containing a part of a domain with not less than 8
 CC amino acids in human CD14 in the region from positions 269-315 in a fully
 CC defined sequence of 356 amino acids as given in the specification. The
 CC antibody is useful in drug compositions for treating sepsis and for
 CC screening remedies for sepsis. This sequence represents an anti-CD14
 CC related protein of the invention

Sequence 356 AA;

Query Match 99.3%; Score 1827; DB 5; Length 356;
 Best Local Similarity 99.4%; Pred. No. 8.5e-168;
 Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDEDFRCVNFSEPOQDMSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 DB 1 TTPEPCELDDEDFRCVNFSEPOQDMSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLRKELTLEDLKITGTMPPPLEA 120
 DB 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLRKELTLEDLKITGTMPPPLEA 120
 QY 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPPALTSL 180
 DB 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPPALTSL 180
 QY 181 DLSNDPGLGERGLMAALCPHKFPFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
 DB 181 DLSNDPGLGERGLMAALCPHKFPFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRAFPQDELP 300
 DB 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRAFPQDELP 300
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
 DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356

RESULT 13
 AAW41693

CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.8e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDPRFCVNFSEPODSEAFQCVSAVEIHAGLNLEPFLKRYDADADP 60
Db 20 TTPEPCELDDPRFCVNFSEPODSEAFQCVSAVEIHAGLNLEPFLKRYDADADP 79

QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPPLEA 139

QY 121 TGLALSSLRRLNVSWATGRSMLAEQWLKPLKVLISIAQHSAPFSYEQVRAFPALTSL 180
Db 140 TGLALSSLRRLNVSWATGRSMLAEQWLKPLKVLISIAQHSAPFSYEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMETPTGVCALAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMETPTGVCALAAGVOPHSLDLSHN 259

QY 241 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 10
ADE55388
ID ADE55388 standard; protein; 375 AA.
XX
AC ADE55388;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein CAA29999, SEQ ID NO 1203.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN W02003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAA29999.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat

or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.8e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDPRFCVNFSEPODSEAFQCVSAVEIHAGLNLEPFLKRYDADADP 60
Db 20 TTPEPCELDDPRFCVNFSEPODSEAFQCVSAVEIHAGLNLEPFLKRYDADADP 79

QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPPLEA 139

QY 121 TGLALSSLRRLNVSWATGRSMLAEQWLKPLKVLISIAQHSAPFSYEQVRAFPALTSL 180
Db 140 TGLALSSLRRLNVSWATGRSMLAEQWLKPLKVLISIAQHSAPFSYEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMETPTGVCALAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMETPTGVCALAAGVOPHSLDLSHN 259

QY 241 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 11
ADD89019
ID ADD89019 standard; protein; 375 AA.
XX
AC ADD89019;
XX
DT 29-JAN-2004 (first entry)
XX
DE TAT258.
XX
KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;
KW cancer.
XX
OS Homo sapiens.
XX

PN W0200235236-A1.
 XX 02-MAY-2002.
 XX 26-OCT-2001; 2001WO-FR003352.
 XX 27-OCT-2000; 2000FR-00013883.
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX Jeannin P, Magistrelli G, Herbault N, Bonnefoy J;
 PI WPI: 2002-383586/41.
 DR N-PSDB; ABN83319.
 XX
 PT Identifying agent that binds to scavenger receptors and signals through a
 PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
 PT cytotoxic T cell response.
 XX
 PS Disclosure; Page 62-63; 71pp; French.
 XX
 CC The present invention relates to a method for identifying new therapeutic
 CC compounds (I) by selecting molecules that bind to scavenger receptors and
 CC signal through a Toll receptor. The present sequence is the protein
 CC sequence for human CD14, which was used to illustrate the method of the
 CC invention. (I) are useful as carriers and/or adjuvants in prophylactic or
 CC therapeutic vaccines, particularly where the antigen is derived from a
 CC virus, bacterium, yeast, fungus, parasite or tumour cell, especially a
 CC pathogen that causes respiratory tract infection, also more generally for
 CC inducing an immune response. (I) can also be used for specific targeting
 CC of active agents (antigens etc.) to antigen-presenting cells (especially
 CC immature dendritic cells), for subsequent internalisation by these cells
 CC.
 SQ Sequence 375 AA;
 Query Match 99.5%; Score 1831; DB 5; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPPECELDDEDFRCVNCNFSFPQDWEAFQVSAVEVEIHAGGVLNLEPFLKRVYDADADP 60
 Db 20 TTPPECELDDEDFRCVNCNFSFPQDWEAFQVSAVEVEIHAGGVLNLEPFLKRVYDADADP 79
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLEA 120
 Db 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLEA 139
 QY 121 TGLALSSLRNNSWATGRSWLAELQWLKPKLVLSIAQHSFAPSVQVRAPFALTSL 180
 Db 140 TGLALSSLRNNSWATGRSWLAELQWLKPKLVLSIAQHSFAPSVQVRAPFALTSL 199
 QY 181 DLSNPGLGERGLMAALCPHKFPAIONLALNTQMETPTGVCALAAGVQPHSLDLSHN 240
 Db 200 DLSNPGLGERGLMAALCPHKFPAIONLALNTQMETPTGVCALAAGVQPHSLDLSHN 259
 QY 241 SLRATNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAQPDPDEL 300
 Db 260 SLRATNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAQPDPDEL 319
 QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
 Db 320 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 375
 RESULT 9
 ADD25617
 ID ADD25617 standard; protein; 375 AA.
 XX
 AC ADD25617;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #86.

XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX
 XX US2003118592-A1.
 XX
 PD 26-JUN-2003.
 XX
 PF 25-JUL-2002; 2002US-00207655.
 XX
 PR 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 XX (GENE-) GENECRAFT INC.
 XX
 PA Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX
 XX WPI: 2003-801317/75.
 XX
 PT New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 178; 157pp; English.
 XX
 CC The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID

PT Recombinant DNA encoding myelomonocytic differentiation antigen CD14 -
 PT used for producing recombinant CD14 for use in e.g. diagnosis of myeloid
 PT disorders such as leukaemia.

XX Claim 1; Fig 3; 11pp; English.

XX Human myelomonocytic differentiation antigen CD14 (AA05316) is an
 CC antigen useful in the diagnosis of mature myeloid leukemia. Its amino
 CC acid sequence was deduced from a cDNA clone (AA139717) obtd. by screening
 CC COS 7 cell transfectants with monoclonal antibodies to CD14. Large ants.
 CC of CD14 can be produced by expression in transformed host cells; mature,
 CC glycosylated CD14 is produced in mammalian host cells, and
 CC nonglycosylated CD14 in prokaryotic hosts. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 2; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
 Db 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLPLEA 120
 Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLPLEA 139
 QY 121 TGLALSRLRNVSATGRSWLAELQWLKPLGVLSIAQAHSPAFSVEQVRAPFALTS 180
 Db 140 TGLALSRLRNVSATGRSWLAELQWLKPLGVLSIAQAHSPAFSVEQVRAPFALTS 199
 QY 181 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 240
 Db 200 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPELP 300
 Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
 Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 7

AAG68129
 ID AAG68129 standard; protein; 375 AA.

XX AAG68129;

AC AAG68129;

DT 23-JAN-2002 (first entry)

DE Human CD14 related protein sequence SEQ ID NO:3.
 XX Human; Toll like receptor; TLR; CD14; antibody; anti-CD14 antibody;
 KW TLR/CD14 binding inhibitor; antibacterial; immunosuppressive;
 KW antipyrretic; hypertensive; immunostimulant; haemostatic; vasotropic;
 KW bacterial infection; sepsis; fever; hypotension; leukopenia;
 KW thrombopenia; shock; multi-organ failure.

XX Homo sapiens.

OS WO200172993-A1.

PN 04-OCT-2001.

PD 02-APR-2001; 2001WO-JP002869.

XX 31-MAR-2000; 2000JP-00099617.

PR 22-NOV-2000; 2000JP-00356719.

PR 28-MAR-2001; 2001US-00806159.

XX (MOCH) MOCHIDA PHARM CO LTD.

PA Furusako S, Mori S, Shirakawa K, Takahashi T;

PI N-PSDB; AAI71230.

XX WPI; 2001-616487/71.

XX Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll
 PT -like receptor, applicable in drugs for treating bacterial infection as
 PT well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.

XX Disclosure; Page 156-160; 202pp; Japanese.

XX The present invention describes an anti-CD14 antibody, which has a
 CC function of inhibiting the binding of CD14 to the Toll-like receptor
 CC (TLR). The anti-CD14 antibody can specifically recognise the epitope
 CC containing the domain from numbers 269-315 in human CD14 of the sequence
 CC in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial,
 CC immunosuppressive, antipyrretic, hypertensive, immunostimulant,
 CC haemostatic and vasotropic activities. The antibody together with other
 CC polypeptides are applicable in drugs for treating bacterial infection as
 CC well as sepsis, fever, hypotension, leukopenia, thrombopenia, shock and
 CC multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295
 CC represent sequences used in the exemplification of the present invention

XX Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 4; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
 Db 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLPLEA 120
 Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLPLEA 139
 QY 121 TGLALSRLRNVSATGRSWLAELQWLKPLGVLSIAQAHSPAFSVEQVRAPFALTS 180
 Db 140 TGLALSRLRNVSATGRSWLAELQWLKPLGVLSIAQAHSPAFSVEQVRAPFALTS 199
 QY 181 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 240
 Db 200 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPELP 300
 Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
 Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 8

ABB83163

ID ABB83163 standard; protein; 375 AA.

XX ABB83163;

DT 09-AUG-2002 (first entry)

XX Human CD14.

XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
 KW cytostatic; immunostimulatory; scavenger receptor; Toll receptor;
 KW respiratory tract infection; CD14.

OS Homo sapiens.

XX

```

Db 121 TGLALSSLRNRVSWATGRSMLAEQQLKPKGLKVLSTIAQAHSPAFSCQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPATQNLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNDPGLGERGLMAALCPHKFPATQNLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SURATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 241 SURATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356

RESULT 5
AAB73984
ID AAB73984 standard; protein; 356 AA.
XX
AC AAB73984;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human soluble CD14 protein.
XX
KW Human; CD14; soluble; fractional quantification; septicemia; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200122085-A1.
XX
PP- 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-JP006359.
XX
PR 17-SEP-1999; 99JP-00264474.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
XX
PI Furusako S, Shirakawa K;
XX
DR WPI; 2001-258042/26.
XX
CC The present sequence is a soluble human CD14 protein. It is provided in a
CC specification relating to a highly-sensitive, convenient and specific
CC method for fractional measurement of a soluble CD14 protein having a low
CC molecular weight in a body fluid. The method comprises measuring total
CC soluble CD14 proteins, measuring a specific soluble CD14 protein having a
CC high molecular weight, and subtracting the value of the measurement of
CC the total proteins by that of the specific protein. The method is useful
CC for the fractional quantitation of a soluble CD14 protein having a low
CC molecular weight in a body fluid. It is also useful for the qualitative
CC and quantitative determination of soluble CD14 protein having a high
CC molecular weight, which is applicable in diagnosis of septicemia
XX
SQ Sequence 356 AA;

Query March 99.5%; Score 1831; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 3.5e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADDP 60
Db 1 TTPEPCELDDDFRCVNFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADDP 60
QY 61 RQYADTVKALRVRLTVGAAGVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120

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Db 61 RQYADTVKALRVRLTVGAAGVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
QY 121 TGLALSSLRNRVSWATGRSMLAEQQLKPKGLKVLSTIAQAHSPAFSVEOVRAFPALTSL 180
Db 121 TGLALSSLRNRVSWATGRSMLAEQQLKPKGLKVLSTIAQAHSPAFSVEOVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPATQNLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNDPGLGERGLMAALCPHKFPATQNLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SURATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 241 SURATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356

RESULT 6
AAW05316
ID AAW05316 standard; protein; 375 AA.
XX
AC AAW05316;
XX
DT 25-MAR-2003 (revised)
DT 03-JAN-1997 (first entry)
XX
DE Myelomonocytic differentiation antigen CD14.
XX
KW Myelomonocytic differentiation antigen; CD14; myeloid leukaemia;
KW diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Modified-site 37..39 /label= Sig_peptide
FT Modified-site /label= Glycosylation
FT Modified-site /note= "potential N-linked glycosylation site"
FT Modified-site 151..153 /label= Glycosylation
FT Modified-site /note= "potential N-linked glycosylation site"
FT Modified-site 266..268 /label= Glycosylation
FT Modified-site /note= "potential N-linked glycosylation site"
FT Modified-site 282..284 /label= Glycosylation
FT Modified-site /note= "potential N-linked glycosylation site"
FT Modified-site 323..325 /label= Glycosylation
FT Modified-site /note= "potential N-linked glycosylation site"
XX
US5543303-A.
XX
PD 06-AUG-1996.
XX
PF 13-DEC-1993; 93US-00165583.
XX
PR 28-NOV-1988; 88US-00276794.
PR 08-JUN-1990; 90US-00536163.
PR 06-NOV-1991; 91US-00787763.
PR 22-JUL-1992; 92US-00916806.
XX
PA (GOYE/) GOYERT S M.
XX
PI Goyert SM;
XX
DR WPI; 1996-370638/37.
DR N-PSDB; AAT39716, AAT39717.
XX

```

KW antiarteriosclerotic; vulnerary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.
 XX Homo sapiens.
 XX WO2003018621-A2.
 XX 06-MAR-2003.
 XX 23-AUG-2002; 2002WO-GB003892.
 XX 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX WPI; 2003-290046/28.
 DR N-PSDB; ADD18697.
 XX New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX Claim 25; SEQ ID NO 127; 424pp; English.
 XX This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.
 XX Sequence 375 AA;

Query Match 100.0%; Score 1840; DB 7; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.1e-169;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDFRCVNCNFSFPQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 DB 20 TTPEPCELDDDFRCVNCNFSFPQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVADADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 DB 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 139
 QY 121 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAOAHSPAFSVEQVRAFPALTSL 180
 DB 140 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAOAHSPAFSVEQVRAFPALTSL 199
 QY 181 DLSNDPGLGERGLMAALCPHFPAQNLALNTGNETPTGVCAALAAAGVOPHSLDLGHN 240
 DB 200 DLSNDPGLGERGLMAALCPHFPAQNLALNTGNETPTGVCAALAAAGVOPHSLDLGHN 259
 QY 241 SLRATVNSAPRCMSSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPODEL 300
 DB 260 SLRATVNSAPRCMSSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPODEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSCTLLVLLQARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSCTLLVLLQARGFA 375
 RESULT 4
 AAG68127
 ID AAG68127 standard; protein; 356 AA.
 XX AC
 XX AAG68127;
 XX 23-JAN-2002 (first entry)
 XX Human CD14 amino acid sequence SEQ ID NO:1.
 XX Human, Toll like receptor; TLR; CD14; antibody; anti-CD14 antibody;
 KW TLR/CD14 binding inhibitor; antibacterial; immunosuppressive;
 KW antipyretic; hypertensive; immunostimulant; haemostatic; vasotropic;
 KW bacterial infection; sepsis; fever; hypotension; leukopaenia;
 KW thrombopaenia; shock; multi-organ failure.
 XX Homo sapiens.
 OS WO200172993-A1.
 XX 04-OCT-2001.
 XX 02-APR-2001; 2001WO-JP002869.
 PF 31-MAR-2000; 2000JP-00099617.
 PR 22-NOV-2000; 2000JP-00356719.
 PR 28-MAR-2001; 2001US-00806158.
 XX (MOCH) MOCHIDA PHARM CO LTD.
 FA Furusako S, Mori S, Shirakawa K, Takahashi T;
 PI WPI; 2001-616487/71.
 DR Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll
 XX -like receptor, applicable in drugs for treating bacterial infection as
 PT well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.
 XX Claim 1; Page 153-155; 202pp; Japanese.

The present invention describes an anti-CD14 antibody, which has a
 CC function of inhibiting the binding of CD14 to the Toll-like receptor
 CC (TLR). The anti-CD14 antibody can specifically recognise the epitope
 CC containing the domain from numbers 269-315 in human CD14 of the sequence
 CC in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial,
 CC immunosuppressive, antipyretic, hypertensive, immunostimulant,
 CC haemostatic and vasotropic activities. The antibody together with other
 CC polypeptides are applicable in drugs for treating bacterial infection as
 CC well as sepsis, fever, hypotension, leukopenia, thrombopenia, shock and
 CC multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 356 AA;

Query Match 99.5%; Score 1831; DB 4; Length 356;
 Best Local Similarity 99.7%; Pred. No. 3.5e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDFRCVNCNFSFPQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 DB 1 TTPEPCELDDDFRCVNCNFSFPQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 DB 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 QY 121 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAOAHSPAFSVEQVRAFPALTSL 180

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 126 Seconds
(without alignments)
798.309 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTPPCLEDDERFCVNF.....TLISGVSGTLLVLLQGARGFA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 29Jan04:.*
1: genesep1980s:.*
2: genesep1990s:.*
3: genesep2000s:.*
4: genesep2001s:.*
5: genesep2002s:.*
6: genesep2003as:.*
7: genesep2003bs:.*
8: genesep2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1840	100.0	375	2 AAW60854	AAW60854 Human CD1
2	1840	100.0	375	3 AAY53878	AAY53878 A human C
3	1840	100.0	375	7 ADD18696	ADD18696 Human dis
4	1831	99.5	356	4 AAG68127	AAG68127 Human CD1
5	1831	99.5	356	4 AAB73984	AAB73984 Human sol
6	1831	99.5	375	5 AAW05316	AAW05316 Myelomono
7	1831	99.5	375	4 AAG68129	AAG68129 Human CD1
8	1831	99.5	375	5 ABB83163	ABB83163 Human CD1
9	1831	99.5	375	7 ADD25617	ADD25617 Binding d
10	1831	99.5	375	7 ADE55388	ADE55388 Human Pro
11	1831	99.5	375	7 ADD89019	ADD89019 TAT258. 1
12	1827	99.3	356	5 AAO22313	AAO22313 Anti-CD14
13	1826	99.2	375	5 AAW41693	AAW41693 Human CD1
14	1807	98.2	431	3 AAB58147	AAB58147 Lung canc
15	1791	97.3	348	2 AAR98576	AAR98576 CD14 sequ
16	1766	96.0	348	2 AAW00467	AAW00467 Soluble C
17	1764	95.9	348	2 AAW00469	AAW00469 Soluble C
18	1764	95.9	348	2 AAW00473	AAW00473 Soluble C
19	1763	95.8	348	2 AAW00470	AAW00470 Soluble C
20	1763	95.8	348	2 AAW00472	AAW00472 Soluble C
21	1763	95.8	348	2 AAW00471	AAW00471 Soluble C
22	1763	95.8	348	2 AAW00468	AAW00468 Soluble C
23	1632	88.8	339	7 ADD29966	ADD29966 Human mod
24	1611	87.6	318	2 AAW00474	AAW00474 Soluble C
25	1577	85.7	307	4 AAG68131	AAG68131 TLR/CD14

26	1577	85.7	307	5 AAO22337	AAO22337 Anti-CD14
27	1575	85.6	307	4 AAG68132	AAG68132 TLR/CD14
28	1575	85.6	307	5 AAO22338	AAO22338 Anti-CD14
29	1561	84.8	331	7 ADD29971	ADD29971 Human mut
30	1462	79.5	285	4 AAG68130	AAG68130 TLR/CD14
31	1462	79.5	285	5 AAO22336	AAO22336 Anti-CD14
32	1420	77.2	407	4 ABO21343	ABO21343 Novel hum
33	1328.5	72.2	373	2 AAW60853	AAW60853 Bovine CD
34	1328.5	72.2	373	3 AAY53877	AAY53877 A bovine
35	1326.5	72.1	377	3 AAY53880	AAY53880 A rabbit
36	1136.5	61.8	366	2 AAW60855	AAW60855 Mouse CD1
37	1136.5	61.8	366	3 AAY53879	AAY53879 A murine
38	1136.5	61.8	366	6 ABU79108	ABU79108 CD14 rece
39	1136.5	61.8	366	7 ADC9867	ADC9867 Murine CD
40	765	41.6	152	2 AAW00476	AAW00476 Soluble C
41	765	41.6	152	2 AAW00480	AAW00480 Soluble C
42	764	41.5	152	2 AAW00478	AAW00478 Soluble C
43	764	41.5	152	2 AAW00477	AAW00477 Soluble C
44	764	41.5	152	2 AAW00479	AAW00479 Soluble C
45	763	41.5	152	2 AAW00475	AAW00475 Soluble C

ALIGNMENTS

RESULT 1

AAW60854
ID AAW60854 standard; protein; 375 AA.

XX AAW60854;

XX 01-OCT-1998 (first entry)

XX Human CD14 protein.

XX CD14; B cell activator; bovine lactation-associated immunotropic protein;
XX LAIT; T cell immunodeficiency; X-linked hyper-IgM syndrome; allergy;
XX common variable immunodeficiency; X-linked agammaglobulinaemia; vaccine;
XX infant feeding formulae; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 87 /note= "encoded by TGC"

XX WO9822580-A2.

XX 28-MAY-1998.

XX 18-NOV-1997; 97WO-CA000880.

XX 18-NOV-1996; 96US-00746883.

XX (WELL-) WELLESLEY HOSPITAL FOUND.

XX Julius MH, Philipp D, Alizadeh-Khiavi K;

XX WPI; 1998-312466/27.

XX N-ESDB; AAV37228.

XX New bovine polypeptide that activates mammalian B cell(s) - used e.g. to
XX treat T cell immunodeficiency or allergy, as vaccine adjuvant, as T cell
XX surrogate for infants, and for monoclonal antibody production, also
XX specific antibodies for treating B cell hyperactivity.

XX Claim 14; Fig 7; 64pp; English.

XX This sequence is the human CD14 protein of the invention. The CD14
XX protein was used to isolate the bovine CD14 of the invention, which is
XX able to activate mammalian B cells. The protein is also known as bovine
XX lactation-associated immunotropic protein (LAIT), and is used to activate
XX B cells, particularly in humans. Particularly it is administered to

this Page Blank (uspto)

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Qy 73 RRLTVGAQVPAQLLVGALRVLAYSRILKELTLEDKITGTMPPLPLEATGLALSSLRN 132
Db 81 RRTRIG-NQNP-EFVGSL--VNLRLASFNASRFYLPGFIPAL----- 120
Qy 133 VSWATGRSWLAELQQLWPKGLKVLISIAQAHSFAPFQVRAFPALTSLDLSNDFGLGERG 192
Db 121 ----FGSLLT-----LEVLDLSSCSITGTIPESLTRLSHLKVLDSLKNAINGD-- 165
Qy 193 LMAALCPHKFPATQNLALRNTGTMETPTGVCALAAAGVQPHSLDLSNLRATVNPAPR 252
Db 166 ----IPLSLTSLQNLGILDSSNVFSGIPANIGALSKLQRLNLSRNLTLTSSIPPSLGD 220
Qy 253 CMWSSALNSLNFAGLE-QVP---KGLPAKLRLVLDLSNRLNRAPOPD----- 297
Db 221 L---SVLIDLSPNGSGSVPSDLKGL-RNLQTLVIAGNRLSGSLPPDLFSLLSKLQII 276
Qy 298 -----ELPEVDNLTLDGNPF--LVPGTALPHEGSMN 326
Db 277 DFRSGFGIALPSRLWSLPKFLDISGNHFSMDLNPNTVTSFSDTVS 323

RESULT 15
D84434
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84434
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84434
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1008 <SIO>
A:Cross-references: GB:AE002093; NID:96598459; PIDN:AACT8507.2; GSPDB:GN00139
C:Genetics:
A:Gene: At2g0220
A:Map position: 2

Query Match 6.5%; Score 120.5; DB 2; Length 1008;
Best Local Similarity 25.2%; Pred. No. 0.2;
Matches 67; Conservative 36; Mismatches 72; Indels 91; Gaps 16;

Qy 94 LAYSRLKELTLEDKITGTMPPLPLEATGLALSS---LRLRVSW--ATGR--SWLAELQ 146
Db 412 LHFEKLVVAVNCRLTGSMRW-----LSSNELQLDLNRLTGAIPSWIGD-- 461
Qy 147 QWLKPGKLVLSIAQAHSFAPFQVRAFPALTSLDLSNDFGLGERGLMAALCPHKFPAIQ 206
Db 462 -----FKALFYLDLSNNSFTGE-----IPKSLTKLE 487
Qy 207 NLALRNTGMEPTG-----VCAALAAAGVQ-----PHSLDLSNLRATVNPAPRCM 254
Db 488 SLTRNLISVNEPSPDPFFPMKRNESARALQVNIQIFGFPPTIELGHNNL-----SGP--I 539
Qy 255 WS-----SALNSLNSFAGLE-QVPKGLP--AKLVLDSLNCNRLNRAFPQDPEVDNLT 306
Db 540 WEEFGNLKLVHFDLKNALSGSIPSSLSGMTSLEALDLSNRLS-GSIPVSLQQLSFL- 597
Qy 307 LDGNPFVPGTALPHEGSMNSGVVPA 332
Db 598 ---SKFSVAYNNL-----SGVIPS 613
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Search completed: October 4, 2004, 16:54:20
Job time : 46 secs

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C:Accession: S42799; I37407

R:Birnbaum, D.

submitted to the EMBL Data Library, July 1993

A:Reference number: S42799

A:Accession: S42799

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662

R:Ollendorff, V.; Noguchi, T.; deLapeyriere, O.; Birnbaum, D.

Cell Growth Differ. 5, 213-219, 1994

A:Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain

A:Reference number: I37407; MUID:94235567; PMID:8180135

A:Accession: I37407

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-662 <RES>

A:Cross-references: EMBL:224680; NID:9439295; PIDN:CAA80847.1; PID:9439296

C:Genetics:

A:Gene: GDB:GARP; D118833E

A:Cross-references: GDB:433911

A:Map position: 11q13.5-11q14

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F:316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F:340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>

F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>

F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>

Query Match 6.7%; Score 124; DB 2; Length 662;

Best Local Similarity 26.1%; Pred. No. 0.06;

Matches 84; Conservative 38; Mismatches 90; Indels 110; Gaps 17;

QY 75 LTVGAA-----QVFAQLLVGALRVLAYSRLKELTLEDLKITGTMPPLEATGLAISLR 129

DB 12 LTLGLAAHQDKVPCMYD-----KVSQVGLGLQVPSVLPDPDTLDSNQ 60

QY 130 LRVSWATGRSWLAELQ-----QWLKPG-----LKVLSIAQ---AHSFAPSYEQ 170

DB 61 LRSI-LASPLGFYTLARHLDTSTNEISFLOPQAFQALTHLEHLSLAHRLAMATLSAGG 119

QY 171 VRAPPALTSLSLSDN---PGLGERGLMAALCPHKPEPAIQNAL-----RNTGMEPT 218

DB 120 LGPIPRVTSLSLDSNLSYSGLLERLLGEA-----PSLHTLSLAENSUTLRTHTFRDMP 173

QY 219 TGVCAALAAAGVQPHSLDLSHNSLRATVNPISA---PRCMSSALNSLNSFAGLEQVPK 274

DB 174 -----AL-----EQDL-LHSNVLMDIEDGAFGLPR-----LTHNLRSNLSLTCSID 214

QY 275 GLPAKLRVLDLSCNRL---NRAPQPD-----ELPEVDNLTLDG 309

DB 215 FSLQQLRVLDLSCNSIEAFATSQPQAFQLTWLDLRENKLLHFPDLAALPRLLIYLNLSN 274

QY 310 NPEIIVP-----GTALPHSG 323

DB 275 NLIRLTPGPPQDSKGIHAPSEG 296

RESULT 13

JC5239

insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)

C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997

C:Accession: JC5239

R:Delhanty, P.; Baxter, R.C.

Biocchem. Biophys. Res. Commun. 227, 897-902, 1996

A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like

A:Reference number: JC5239; MUID:97040714; PMID:8886027

A:Contents: liver

A:Accession: JC5239

A:Molecule type: mRNA

A:Residues: 1-605

C:Comment: This factor is structurally related to proinsulin and have insuline-like metal

Query Match 6.7%; Score 122.5; DB 2; Length 605;

Best Local Similarity 25.1%; Pred. No. 0.071;

Matches 103; Conservative 51; Mismatches 158; Indels 99; Gaps 22;

QY 8 LDEDFRCVCFSEPPDPWSE-----AFQCVSAVEVEIHAGG--LNLEPFLKRVDA 58

DB 161 LEDGLFEGLGNLDNLGWSLAVLPDAAFRGGLGRLVLAGNRLAYLQPAL--FSGLA 218

QY 59 DPRQYADTVKALRVRLTVGAAQVPA-----QLLVGALRVLAYSRLKELTLEDL---K 108

DB 219 ELRELDLSRNALRAIKANV-FAQLPRLQKLYLDRLNLTAAVAPGAPGLKALRWLDLSNR 277

QY 109 ITG-----TMPPL-----PLEATGLALSRLRN-----SWATGRSWLAELQWLKPL 153

DB 278 VAGLEDTFPGLLGLRVLRSHNAISLRPTFDLHLELQGHNRIRQLAERSFGL 337

QY 154 KVLISIAQHSFAPSYEQVRAFPALTS---LDLSDN-----PGLG-----ERGL 193

DB 338 QQLVLTLDHNLQEVKVGAFGLTNVAVMLSGNCLRNLPQEVFRGLKLSLHLEGG 397

QY 194 MAALCPHKF---PAIQNALRNTGM-----ETPTGVCAALAAAGVQ-----PHSLD--- 236

DB 398 LGRIPTHFAGLSGLRLFLKDNGLVGIEQSLMGLAELELDLTSNQLTHLPQOLFOGL 457

QY 237 -----LSHN---SLRATVNPSPRCMSSALNSLNSFAGLEQVPKLPA---KLRLV 283

DB 458 GKLEVLILLSHNRLELPADALGPLQRAFW-----LOVSHNRLEALPQSLASGLRLYL 511

QY 284 DLSCNLRN-APQDELPVDNLTLDGPNP--LVPGTALPHEGSMNSGVVP 331

DB 512 NLNRNSLRTFTFPQ---PGLRLWLEGNPMDSCPLKALRDFALQNPSAVP 559

RESULT 14

T08575

protein kinase homolog T22F8.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Mar-2000

C:Accession: T08575

R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Maye

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16442

A:Accession: T08575

A:Molecule type: DNA

A:Residues: 1-864 <BEV>

A:Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.170

A:Experimental source: cultivar Columbia; BAC clone T22F8

C:Genetics:

A:Gene: ATSP:T22F8.170

A:Map position: 4

A:Introns: 632/2; 675/2; 683/1

C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; p

Query Match 6.6%; Score 121.5; DB 2; Length 864;

Best Local Similarity 24.0%; Pred. No. 0.13;

Matches 69; Conservative 40; Mismatches 101; Indels 77; Gaps 12;

A:Gene: At2g27060
A:Map position: 2

Query Match 7.4%; Score 136.5; DB 2; Length 1007;
Best Local Similarity 22.8%; Pred. No. 0.01;
Matches 85; Conservative 53; Mismatches 131; Indels 103; Gaps 18;

QY 49 PELKRVDA-DADPRQYADTV-----KALVRRLTVGAAQVPAQL----- 86
DB 226 PFDDLEVPDASSNQLSGSVFVSFKILRLQDNQNSASLPGLLQESSITLTDLDL 285

QY 87 ----LVGALRVLAYSLKELTLEDKITGTMPLEATGALSSILRLNRSWATGRSML 142
DB 286 SINQLEGPIGTSITSTLEKINSSNLSGS---LPLKVGHCAIIDLNNKIS-----GEL 337

QY 143 AELQW-----LKPQ-----LKVLSIAQAHSAPFSYQVRAF-----PA 176
DB 338 SRIQNWGDSVEIIRLSSNSLTGLPQTSQFRLRTSLKAANN---SLQCVLPFILGTYP 394

QY 177 LTSLDLSDNPGGLGERGLMAALCPHF---PAIQNALRLNTGNETPTGVCAALAAAGVQPH 233
DB 395 LXEIDLINQ-----LSGVIPSNLFISAKITELNLSNNNFGSLPLQDASTVGNLSLT 447

QY 234 SLDSLHSLRATVNPSPRCMWSALNSLISFAGLE-QVPKGLPAKLRVLDLSCNRLNR 292
DB 448 NIGLSHSLGGVLSLELTR---FHNLSLISLXNNFEGNIPDGLPDSLKMTFVSANNLS- 503

QY 293 APQDELPE-----VDNLTLDGNPFLVPGTALP-----HSGMNSGVVPACARST 337
DB 504 ----GNVPENLRFPDSAFHGNALLNVPISLPKDKTITLRKHGYHMKTSV-----KAA 554

QY 338 LSVG-VSGTLVL 348
DB 555 LIIGLVGTALL 566

RESULT 7
AG0123
Probable antigenic leucine-rich repeat protein YPO1007 [imported] - Yersinia pestis (str
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0123
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-605 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89850.1; PID:gl5979076; GSPDB:GN00175
C:Genetics:
A:Gene: YPO1007

Query Match 7.2%; Score 132; DB 2; Length 605;
Best Local Similarity 23.6%; Pred. No. 0.012;
Matches 69; Conservative 41; Mismatches 78; Indels 104; Gaps 14;

QY 76 TVGAAQVPA-----QLLVGALRVLAYSLKE-----LTLEDKITG--- 111
DB 26 TSTAALTADYIATWEKWDNPRIVAGQEQVARMKECLENTERTLDDLDLGLSLPD 85

QY 112 TMPPLEATGLASSLRNRSWATGRSWLAELQOMLPGLKVLISIAQAHSAPFSYEQV 171
DB 86 TLPPCN-----KLNII---ENKLTLPPTLPDNLQTLNAA-----ENQL 121

QY 172 RAFF-----ALTSIDLSDNPGCLGERGLMAALCPHFPA- 204
DB 122 RTLNTLTPASLLSNVYGNELERLPESLPEGLKKLDVGRNESLQR-----ENRLPPN 173

QY 205 IQNLALRNTGM-ETPTGVCAALAAAGVQPHS---LDLSHSLRATVNPSPRCMWSALN 260

DB 174 LESLGMANCRLELTPT-----LPNSLEKLEVNDNQHL-TLPDTLP-----ALIS 216

QY 261 SINLSFAGLEQVPGKLPKLRVLDLSCNLRNAPQDELPEVDNLTLDGNPF 312
DB 217 SLVSSNRLTALPENLPGLSDIYAKDNQLSQLPDLAHLPONCSRILDGNPF 268

RESULT 8
TI0636
Hypothetical protein T13K14.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: TI0636
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke,
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: TI0636
A:Molecule type: DNA
A:Residues: 1-1143 <BEV>
A:Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.100
A:Experimental source: cultivar Columbia; BAC clone T13K14
C:Genetics:
A:Gene: ATSP:T13K14.100
A:Map position: 4
A:Introns: 334/1; 815/2; 941/3; 970/2; 1006/3; 1031/1; 1073/3; 1105/3

Query Match 7.0%; Score 129; DB 2; Length 1143;
Best Local Similarity 24.0%; Pred. No. 0.049;
Matches 93; Conservative 42; Mismatches 115; Indels 138; Gaps 19;

QY 30 PQCVSAVEV-BIHA-----GGLNLEPFL-----KRYDADADPRQYADTVKAL-----RVRL 75
DB 194 FELISSLEVLDLHGNSIDGNLDGEFFLLTNASYVDISN-RLVTTSGKLLPGVSESIKHL 252

QY 76 TVGAAQVPAQLLVG-----ALRVLAIS-----RLKELTLEDKITGTMP 115
DB 253 NLSHNLQSGTSFGFQFNKLVLDLNSMLSGELPGFNYYVDLEVLKLSNRFSGSLPN 312

QY 116 LPLEATGLALSSLR-----RNVSWATGRSWLAELQOMLPGLKVLISIAQAHSAPFSYEQVRA 173
DB 313 NLLAKGDSLLTLTDLSSGNLS-----GPNSSIMS----- 341

QY 174 PPAITLSDLSDNPGCLGERGLMAALCPHFPAIQNALRLNTGNETPTGVCAALAAAGVQPH 233
DB 342 -TTLHTLTLSSNSLTGELPLI-----TGCVLLDLSSNNQFE 376

QY 234 S-----LDLSHSLRATVNPSPRCMWSALNSLISFAGL-----EQVPGK 275
DB 377 GNLTRWSKNWENIEYLDLSQNHFTGSPDPATPQLL---RANHLNLSYKNLGTGSLPERIPTH 433

QY 276 LPKLRVLDLSCNLRNAPQDEL---PEVDNLTLDGNPFLVPGTALPHGS----- 324
DB 434 YP-KLRVLDISSNSL-BGPPIGALLSMPTLEEHLQNNGMTGNIGLPSSGSRIRLLDLS 491

QY 325 --MNSGVVPACARSTLSVGVSGLVLILQ 350
DB 492 HNRFDGDLP-----GVFGSLTNLQ 510

RESULT 9
AF0123
Probable antigenic leucine-rich repeat protein YPO1006 [imported] - Yersinia pestis (str
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0123
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0123

F;266-288/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;497-830/Domain: gelsolin repeat homology <GEL1>
F;892-1250/Domain: gelsolin repeat homology <GEL2>

```
Query Match      8.2%; Score 150.5; DB 2; Length 1256;
Best Local Similarity 23.0%; Pred. No. 0.0011;
Matches 92; Conservative 48; Mismatches 103; Indels 157; Gaps 18;

QY 45 LNLPEFLKRVDAAD--PROVADTVKAL-RVRRLTVG---AAQVPAQI----- 86
Db 1 MSVLPPFVRGVDFTKNDFSATFPSSMRQMSRVQWLTDLTQLAETPEELHQLKLEHLSLN 60
QY 87 -----LVGALRVLAYSLKELTLEDKITGTMPPL--PLEATGLALSSLRNRVSWATG 138
Db 61 HNRLEKIFGELTELSCURSDLRHNLQNSGIPPELFHLELTITLDLSHNKLKEVPEGLE 120
QY 139 RSMIAELQWLKPGKLVLSAQAH-----SPAF-----SYQVRAFPFA----- 176
Db 121 RA-----KNLIVNLNSNNQIESIPTPLFTHLTDLFLDLSHNRKLETLPQTRRLI 170
QY 177 -LTSLDLSDNPGIGERGMAALCPHKFPAIONLAL-----RNTGMPETGVCRAALAAAG 229
Db 171 NLKTLDSLHNP-----LELFQRLPSLQSLVLEKMSGTQRTLLNPFPSIDSLANLC- 222
QY 230 VQPHSLDLSHNSLRATVNSAPRCMWS-----SALNSLNL 265
Db 223 -----ELDSLHNSL-----PKLPDCVYVNVTLVRLNLSDELTELTAGVELWQRLS 273
QY 266 -----FAG-----LEQVPKGL- 276
Db 274 RNQVALPAALCKLPKRLRLVNDNKNFEGIPSGIGKGLGALVFSANLLEVMVEGLC 333
QY 277 -PAKLRVLDSLNRINRAPQDELPE-VDNLTLDGNPFLV 314
Db 334 RCGALKQLNLSNRLITLPDAIHLEGLDQLDLRNNPELV 373

*
RESULT 4
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1
```

```
Query Match      7.9%; Score 145; DB 2; Length 786;
Best Local Similarity 24.9%; Pred. No. 0.0016;
Matches 71; Conservative 39; Mismatches 115; Indels 60; Gaps 10;

QY 94 LAYSLKELTLEDKITGTMPPLPLEATGLALSSLRNRVSWATGRSWLAELQ----- 146
Db 216 LELSNIK-CVLEDSKCVFLSILAKLTNPKLSSITLNNIE-TTWNSPFIRILQVWHTV 273
QY 147 -----QWLKGLKVLSTAOAHSPAPSYEQVRAFPALTSLDLSNPG 187
Db 274 WYSSISNVKQGQDLDFRDFYSGTSLKALSILHQVVDVFGFPQSYIIFSNMKNKPTV 333
QY 188 LGERGLMAALCPHKFPAIONLALRN-----TGME-----PTGVC 224
Db 334 SGTR-MVHMLCPKSLPPLHLDFSNLLTDTVFENCGLHTELETILQMNQKLSKIAE 392
QY 225 LAAAGVQPHSLDLSHNSLRATVNSAPRCMWSALNSLNSFAGL-EQVPKGLPAKLRVL 283
Db 393 MTTQMKSLQQLDISQNSV--SYDEKKGDCSWTKSLLSLNMSNLTITDIFRCLPPIKVL 450
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QY 284 DLSCNRLNRP-OPDELPEVDNLTLDGNPFLVPGTALPHEGSMNS 327
Db 451 DLHSNKIKSPKQVVKLEALQELNVAENSL-----TDLPGCGSFSS 491

RESULT 5
T48499
receptor-like protein kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein T28J14.220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48499
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T48499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1192 <BEV>
A;Cross-references: EMBL:AL163652
A;Experimental source: cultivar Columbia; BAC clone T28J14
C;Genetics:
A;Map position: 5
A;Note: T28J14.220

Query Match      7.7%; Score 142; DB 2; Length 1192;
Best Local Similarity 23.9%; Pred. No. 0.0047;
Matches 83; Conservative 48; Mismatches 116; Indels 100; Gaps 14;

QY 77 VGAQVPAQLLVGAL--RVLAYSLKELTLEDKITGTMP-----LPLEATGLALS 126
Db 67 VNSLSLPSLSLRGQIPKEISSLNKRLRELCLAGNFGSKIPPEIWNKHLQTLDSLGNSLT 126
QY 127 SLRLNVSWATGRSWLAELQWLKVLKLSIAQAHSPAPSYEQVRAFPALTSLDLSNP 186
Db 127 GLLP-----LLSELQQLYLDLSDNHFSGSLPPSFFI-----SLPALSSLDVSNNS 173
QY 187 GLGERGLMAALCPHKFPAIONLALRNTGMEPTG-----VCAALAAA-----GVQ 231
Db 174 LSGE-----IPPEIKLSNLSNLYMGLNSFSQIPEISIGNISLLKNFAAPSCFFNGPL 226
QY 232 PH-----SLDLSHNSLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRV 282
Db 227 PKEISKLKLAKLDLSYNPLKCSIPKSGELHNLNLSLVSAELIGLIPPELGNCKSLKS 286
QY 283 LDLSNRLNRPQDELPEV-----DNLTLDGNPFLVPG 316
Db 287 LMLSFNLSL-GPLPLELSEIPLLTFSARNQLSGSLPSWMGKWKVLDLNNRNF---S 342
QY 317 TALPHE-----GSMNSGVVP--ACARSTL-SVGVSGTLV 347
Db 343 GEIPHEIEDCPMLKHLASLNLSSGSLPRELCSGSLAEIDLGNLL 389
```

```
RESULT 6
C84668
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84668
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:1061197
A;Accession: C84668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1007 <STO>
A;Cross-references: GB:A8002093; NID:G3885336; PIDN:AAC77864.1; GSPDB:GN00139
C;Genetics:
```


A:Gene: GDB:CD14
A:Cross-references: GDB:119759; OMIM:158120
A:Map position: 5q31.1-5q31.1
A:Introns: 1/3
C:Superfamily: monocyte surface glycoprotein CD14
C:Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-375/Product: monocyte surface glycoprotein CD14 #status predicted <MAT>
F:20-367/Product: monocyte surface glycoprotein CD14 #status predicted <MAT>
F:91-329/Region: 9-residue repeats (LVV)-X-X-L-X-[LVIIY]-[SRTA]-X-[NAT]
F:37,151,282,323/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1840; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPPECELDDEDFRCVNFSEPPQDMSFAQCVAVEIHHAGGLNLEPFLKRVDAADAP 60
DB 20 TTPPECELDDEDFRCVNFSEPPQDMSFAQCVAVEIHHAGGLNLEPFLKRVDAADAP 79

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
DB 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139

QY 121 TGLALSSLRRLNVSWATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTSL 180
DB 140 TGLALSSLRRLNVSWATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTSL 199

QY 181 DLSNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 259

QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 300
DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 319

QY 301 EVDNLTLDGNPFLVGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 2
TDM54
monocyte surface glycoprotein CD14 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: S03605; A43539; S04967
F:Matsumura, K.; Setoguchi, M.; Nasu, N.; Higuchi, Y.; Yoshida, S.; Yamamoto, S.
Nucleic Acids Res. 17, 2132, 1989
A:Title: Nucleotide and amino acid sequences of the mouse CD14 gene.
A:Reference number: S03605; MUID:89183627; PMID:2467257
A:Accession: S03605
A:Molecule type: DNA
A:Residues: 1-366 <MAT>
A:Cross-references: EMBL:X13987; NID:G50336; PIDN:CAA32166.1; PID:G2342527
F:Ferrero, E.; Hsieh, C.L.; Francke, U.; Goyert, S.M.
J. Immunol. 145, 331-336, 1990
A:Title: CD14 is a member of the family of leucine-rich proteins and is encoded by a gene
A:Reference number: A43539; MUID:90293480; PMID:1694207
A:Accession: A43539
A:Molecule type: DNA
A:Residues: 1-366 <FER>
A:Cross-references: GB:M34510; NID:G192460; PIDN:AAA37387.1; PID:G387121
F:Setoguchi, M.; Nasu, N.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Biochim. Biophys. Acta 1008, 213-222, 1989
A:Title: Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary
A:Reference number: S04967; MUID:89287330; PMID:2472171
A:Accession: S04967
A:Molecule type: mRNA
A:Residues: 1-366 <SET>
A:Cross-references: EMBL:X13333; NID:G50338; PIDN:CAA31710.1; PID:G50339
C:Genetics:

A:Introns: 1/3
C:Superfamily: monocyte surface glycoprotein CD14
C:Keywords: glycoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-366/Product: monocyte surface glycoprotein CD14 #status predicted <MAT>
F:87-323/Region: 9-residue repeats (LVV)-X-X-L-X-[LVIIY]-[SRTA]-X-[NAT]
F:33,147,180,276,317/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.8%; Score 1136.5; DB 1; Length 366;
Best Local Similarity 65.7%; Pred. No. 6.2e-83;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

QY 3 PEPCELDDEDFRCVNFSEPPQDMSFAQCVAVEIHHAGGLNLEPFLKRVDAADAPRQ 62
DB 20 PEPCELDDEES--CSCNFSDDPKPDMSSAFNCLGAADVLYGGGSRLEYLLKRVDTADLQG 77

QY 63 YADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEATG 122
DB 78 FTDIYKLSLKRLLTVRAIRIFSRILFGALRVLGISGQELTLENLEVTGTAPPPLEATG 137

QY 123 LALSRLRLNVSWATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTSLDL 182
DB 138 PDNLNLRLNVSWATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTSLDL 197

QY 183 SDNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHNSL 242
DB 198 SDNPGLGERGLISALCPKLPFTQLVLAIRNAGMETPGVCSCALAAARVQLQGLDLSHNSL 257

QY 243 RATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDELPEV 302
DB 258 RDA--GAPSCDWSQLNSLNSFTGLKQVPGKLPKLRVLDLSCNRLNRAPODDELPEV 315

QY 303 DNLTLDGNPFLVGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGF 355
DB 316 GNLILKGNPFL---DSSESHSEKFNSEVVTAGAPSSQVALSGTLALLGLDLRF 365

RESULT 3
S60461
gene flightless-I protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: S60461; T08425
F:de Couet, H.G.; Fong, K.S.K.; Weeds, A.G.; McLaughlin, P.J.; Miklos, G.L.G.
Genetics 141, 1049-1059, 1995
A:Title: Molecular and mutational analysis of a gelsolin-family member encoded by the fly
A:Reference number: S60461; MUID:96129280; PMID:8582612
A:Accession: S60461
A:Molecule type: DNA
A:Residues: 1-1256 <DEC>
A:Cross-references: GB:AF017777; EMBL:U28044; NID:G3004652; PIDN:AAC28407.1; PID:G3004661
F:Maleszka, R.; de Couet, H.G.; Miklos, G.L.
Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998
A:Title: Data transferability from model organisms to human beings: insights from the fur
A:Reference number: Z16415; MUID:98188272; PMID:9520435
A:Accession: T08425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1256 <NAL>
A:Cross-references: GB:AF017777; GB:U080043; GB:U28044; NID:G3004652; PIDN:AAC28407.1; PID
C:Genetics:
A:Gene: fli-I; flightless-I
A:Cross-references: FlyBase:FBgn0000709
A:Introns: 18/3; 1070/2; 1120/3
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:53-75/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:76-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:101-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:124-147/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:148-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:171-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:220-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:243-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 41 Seconds
(without alignments)

835.224 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPPCLELDEDFRCVNF.....TLSGVSGTLVLQARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Piri:*

2: Piri2:*

3: Piri3:*

4: Piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1840	100.0	375	1 TDHUM4	monocyte surface g
2	1136.5	61.8	366	1 TDMSW4	monocyte surface g
3	150.5	8.2	1256	2 S60461	gene flightless-1
4	145	7.9	786	2 T08664	Toll protein-like
5	142	7.7	1192	2 T48499	receptor-like prot
6	136.5	7.4	1007	2 C84668	probable receptor-
7	132	7.2	605	2 AG0123	probable antigenic
8	129	7.0	1143	2 T10636	hypothetical prote
9	128	7.0	291	2 AF0123	probable antigenic
10	127.5	6.9	905	2 T00475	probable disease r
11	126.5	6.9	1196	2 T09356	brassinosteroid-in
12	124	6.7	662	2 S42799	garp precursor - h
13	122.5	6.7	605	2 JC5239	insulin-like growt
14	121.5	6.6	864	2 T08575	protein kinase hom
15	120.5	6.5	1008	2 D84434	probable receptor-
16	119	6.5	626	2 AB0123	probable antigenic
17	119	6.5	835	2 T05259	probable disease r
18	119	6.5	890	2 T00800	disease resistance
19	117.5	6.4	858	2 T00258	hypothetical prote
20	117	6.4	987	2 T50850	receptor protein k
21	115.5	6.3	1068	2 H96785	hypothetical prote
22	115	6.2	788	2 AG0785	secreted effector
23	114.5	6.2	1112	2 T10504	disease resistance
24	113	6.1	462	2 D84858	hypothetical prote
25	113	6.1	981	2 T50851	receptor protein k
26	113	6.1	1134	2 T04587	hypothetical prote
27	112.5	6.1	960	2 G84652	probable receptor-
28	112.5	6.1	1389	2 T13852	gene wheeler prote
29	112	6.1	768	2 T17462	disease resistance

30	112	6.1	962	2 T04124	receptor-like prot
31	111.5	6.1	767	2 B84594	probable LRR recep
32	111.5	6.1	1385	2 T13887	tlr protein - frui
33	111	6.0	574	2 B35149	ipaH protein - Shi
34	111	6.0	836	2 T46070	hypothetical prote
35	110.5	6.0	789	2 T52067	hypothetical prote
36	110.5	6.0	1143	2 B84431	probable receptor
37	110	6.0	1029	2 T00712	protein kinase hom
38	110	6.0	2756	2 T30183	hypothetical prote
39	109.5	6.0	679	2 T20713	insulin-like growt
40	109	5.9	605	2 A41915	disease resistance
41	108.5	5.9	853	2 T17461	probable serine/th
42	108.5	5.9	1013	2 T10659	chondroadherin pre
43	107.5	5.8	361	2 A53860	protein F21B7.6 [i
44	107.5	5.8	395	2 A86166	leucine-rich repea
45	107.5	5.8	397	2 T00914	

ALIGNMENTS

RESULT 1

TDHUM4

monocyte surface glycoprotein CD14 precursor - human

N;Alternate names: monocyte differentiation antigen CD14;

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 22-Jun-1999

C;Accession: A27637; S00917; S04968; PLO108; A30555

R;Haziot, A.; Chen, S.; Ferrero, E.; Low, M.G.; Silber, R.; Goyert, S.M.

J. Immunol. 141, 547-552, 1988

A;Title: The monocyte differentiation antigen, CD14, is anchored to the cell membrane b

A;Reference number: A27637; MUID:88258060; PMID:3385210

A;Accession: A27637

A;Molecule type: mRNA

A;Residues: 1-375 <HAZ>

R;Ferrero, E.; Goyert, S.M.

Nucleic Acids Res. 16, 4173, 1988

A;Title: Nucleotide sequence of the gene encoding the monocyte differentiation antigen,

A;Reference number: S00917; MUID:88234022; PMID:2453848

A;Accession: S00917

A;Molecule type: DNA

A;Residues: 1-375 <FBR>

A;Cross-references: EMBL:X06882; NID:g29736; PIDN:CAA29999.1; PID:g312999

R;Setoguchi, M.; Nasu, N.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.

Biochim. Biophys. Acta 1008, 213-222, 1989

A;Title: Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary

A;Reference number: S04967; MUID:89287330; PMID:2472171

A;Accession: S04968

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-186 'C', 188-375 <SET>

A;Cross-references: EMBL:X13334; NID:g29740; PIDN:CAA31711.1; PID:g29741

R;Bazil, V.; Baudys, M.; Hilgert, I.; Stefanova, I.; Low, M.G.; Zbrozek, J.; Horejsi, V.

Mol. Immunol. 26, 657-662, 1989

A;Title: Structural relationship between the soluble and membrane-bound forms of human

A;Reference number: PLO108; MUID:89384684; PMID:2779588

A;Accession: PLO108

A;Molecule type: protein

A;Residues: 362-367 <BAZ>

A;Note: the carboxyl-terminal sequence of the soluble CD14 isolated from urine was dete

R;Simmons, D.L.; Tan, S.; Tenen, D.G.; Nicholson-Weller, A.; Seed, B.

Blood 73, 284-289, 1989

A;Title: Monocyte antigen CD14 is a phospholipid anchored membrane protein.

A;Reference number: A30555; MUID:89088540; PMID:2462937

A;Accession: A30555

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-76 'G', 78-186 'C', 188-375 <SIM>

C;Comment: This glycoprotein is expressed primarily on peripheral blood monocytes and m

C;Comment: The protein is anchored to the cell membrane by a phosphatidylinositol linka

C;Genetics:

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Wed Oct 6 09:56:25 2004

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-60-443-566-2776

Query Match	99.5%	Score 1831	DB 33	Length 375
Best Local Similarity	99.7%	Pred. No. 1.5e-160		
Matches 355	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 1	TTPEPCELDDERFCVNFSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60		
Db 20	TTPEPCELDDERFCVNFSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	79		
QY 61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLPLEA	120		
Db 80	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLPLEA	139		
QY 121	TGLALSSLRIRNVSWATGRSWLAELQWLKGLKVLSTIAQAHSPAFSCEQVRAPALTSL	180		
Db 140	TGLALSSLRIRNVSWATGRSWLAELQWLKGLKVLSTIAQAHSPAFSCEQVRAPALTSL	199		
QY 181	DLSDNPGIGERGLMAALCPHKFPALQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN	240		
Db 200	DLSDNPGIGERGLMAALCPHKFPALQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN	259		
QY 241	SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKURVLDLSCNRLNRAPOPDDEL	300		
Db 260	SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKURVLDLSCNRLNRAPOPDDEL	319		
QY 301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLLQGARGFA	356		
Db 320	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLLQGARGFA	375		

Search completed: October 4, 2004, 17:01:55
Job time : 422 secs

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
 DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 199
 QY 181 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 240
 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
 DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
 QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 356
 DB 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 375

RESULT 13

US-10-331-496A-23
 ; Sequence 23, Application US/10331496A
 ; GENERAL INFORMATION:
 ; APPLICANT: FRANTZ GRETCHEN
 ; APPLICANT: HILLAN, KENNETH J.
 ; APPLICANT: PHILLIPS, HEIDI S.
 ; APPLICANT: POLAKIS, PAUL
 ; APPLICANT: SMITH, VICTORIA
 ; APPLICANT: SPENCER, SUSAN D.
 ; APPLICANT: WILLIAMS, P. MCKEY
 ; APPLICANT: WU, THOMAS D.
 ; APPLICANT: ZHANG, ZEMIN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P5014R1-PCT
 ; CURRENT APPLICATION NUMBER: US/10/331,496A
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 60/345,444
 ; PRIOR FILING DATE: 2002-01-02
 ; PRIOR APPLICATION NUMBER: US 60/351,885
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: US 60/360,066
 ; PRIOR FILING DATE: 2002-02-25
 ; PRIOR APPLICATION NUMBER: US 60/362,004
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/366,869
 ; PRIOR FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: US 60/366,284
 ; PRIOR FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: US 60/368,679
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/404,809
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/405,645
 ; PRIOR FILING DATE: 2002-08-21
 ; NUMBER OF SEQ ID NOS: 95
 ; SEQ ID NO 23
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-331-496A-23

Query Match 99.5%; Score 1831; DB 29; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1.5e-160;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHHAGLNLEPFLKRVADADP 60
 DB 20 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHHAGLNLEPFLKRVADADP 79
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKITGTWPPLEA 120
 DB 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKITGTWPPLEA 139
 QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 180

DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 199
 QY 181 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 240
 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
 DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
 QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 356
 DB 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 375

RESULT 14

US-10-723-860-759
 ; Sequence 759, Application US/10723860
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10/723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 759
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-860-759

Query Match 99.5%; Score 1831; DB 32; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1.5e-160;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHHAGLNLEPFLKRVADADP 60
 DB 20 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEIHHAGLNLEPFLKRVADADP 79
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKITGTWPPLEA 120
 DB 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKITGTWPPLEA 139
 QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
 DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHSPAFSCEQVRAFPALTSL 199
 QY 181 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 240
 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
 DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
 QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 356
 DB 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQARGFA 375

RESULT 15

US-60-443-566-2776
 ; Sequence 2776, Application US/60443566
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann

Db 200 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 10
US-09-791-537-85983
; Sequence 85983, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMEB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85983
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-85983

-Query Match 99.5%; Score 1831; DB 22; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 139
QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 180
Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 199
QY 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 11
US-10-207-655-178
; Sequence 178, Application US/10207655
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 178

; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-178

Query Match 99.5%; Score 1831; DB 28; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 139
QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 180
Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 199
QY 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 12
US-10-219-051B-1203
; Sequence 1203, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 1203
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / CAA29999
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-1203

Query Match 99.5%; Score 1831; DB 28; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPOQDMSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 139

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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-31301-3

Query Match
Best Local Similarity 99.5%; Score 1831; DB 1; Length 375;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
Db 20 TTPECELDDEDFRCVCFNFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 259
QY 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQARGFA 375

RESULT 8
PCT-US02-41798A-23
; Sequence 23, Application PC/TUS0241798A
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHE
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P50141-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/41798A
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 23
; LENGTH: 375

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-41798A-23

Query Match
Best Local Similarity 99.5%; Score 1831; DB 1; Length 375;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
Db 20 TTPECELDDEDFRCVCFNFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 259
QY 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQARGFA 375

RESULT 9
PCT-US03-38193-759
; Sequence 759, Application PC/TUS0338193
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.00PC00
; CURRENT APPLICATION NUMBER: PCT/US03/38193
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 759
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38193-759

Query Match
Best Local Similarity 99.5%; Score 1831; DB 1; Length 375;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
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QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSRLRLNVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240
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301	EV	DN	LT	DG	NP	FL	VP	GT	AL	PHE	G	M	N	S	G	V	V	P	A	C	A	R	S	T	L	S	V	G	S	G	T	L	V	L	L	Q	G	A	R	G	F	A	356	
301	EV	DN	LT	DG	NP	FL	VP	GT	AL	PHE	G	M	N	S	G	V	V	P	A	C	A	R	S	T	L	S	V	G	S	G	T	L	V	L	L	Q	G	A	R	G	F	A	356	
241	SL	RA	T	V	N	P	S	A	P	R	C	W	S	S	A	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	300
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241	SL	RA	T	V	N	P	S	A	P	R	C	W	S	S	A	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	L	N	S	300	
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Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60

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QY 181 DLSNDFGLGERGLMAALCPHKFPALQNLALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
 Db 181 DLSNDFGLGERGLMAALCPHKFPALQNLALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240

QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
 Db 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300

QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
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RESULT 2

US-09-721-904A-5
 ; Sequence 5, Application US/09721904A
 ; GENERAL INFORMATION:
 ; APPLICANT: JULIUS, Michael H.
 ; APPLICANT: FILIPP, Dominik
 ; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
 ; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
 ; FILE REFERENCE: 47841/00063
 ; CURRENT APPLICATION NUMBER: US/09/721.904A
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: PCT/CA99/00482
 ; PRIOR FILING DATE: 1999-05-27
 ; PRIOR APPLICATION NUMBER: US 60/086,884
 ; PRIOR FILING DATE: 1998-05-27
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Wordperfect 9.0
 ; SEQ ID NO 5
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-721-904A-5

Query Match 100.0%; Score 1840; DB 21; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.2e-161;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 Db 20 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 79

QY 61 ROYADVTKALVRRLTVGAQVPAQLLVGALRVLAISRUKELTLEDKLTGTMPPLPLEA 120
 Db 80 ROYADVTKALVRRLTVGAQVPAQLLVGALRVLAISRUKELTLEDKLTGTMPPLPLEA 139

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSL 180
 Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSL 199

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QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
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QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
 Db 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 3

US-09-721-904B-5
 ; Sequence 5, Application US/09721904B
 ; GENERAL INFORMATION:
 ; APPLICANT: JULIUS, Michael H.
 ; APPLICANT: FILIPP, Dominik
 ; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
 ; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
 ; FILE REFERENCE: 47841/00063
 ; CURRENT APPLICATION NUMBER: US/09/721.904B
 ; CURRENT FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: PCT/CA99/00482
 ; PRIOR FILING DATE: 1999-05-27
 ; PRIOR APPLICATION NUMBER: US 60/086,884
 ; PRIOR FILING DATE: 1998-05-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Wordperfect 9.0
 ; SEQ ID NO 5
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-721-904B-5

Query Match 100.0%; Score 1840; DB 21; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.2e-161;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ROYADVTKALVRRLTVGAQVPAQLLVGALRVLAISRUKELTLEDKLTGTMPPLPLEA 120
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QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSL 180
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 Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
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RESULT 4

US-09-791-537-18195
 ; Sequence 18195, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 18195

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 418 Seconds
(without alignments)
831.280 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTPPECELDDEDFRCVCFNS.....TLGVGVGTLVLLQGARGFA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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33: /cgn2_6/ptodata/2/paa/US108 COMB.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	100.0	100.0	356	US-09-807-709A-1	Sequence 1, Appli
2	100.0	100.0	356	US-09-807-709A-1	Sequence 5, Appli
3	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App
4	100.0	100.0	356	US-09-807-709A-1	Sequence 1203, Ap
5	100.0	100.0	356	US-09-807-709A-1	Sequence 23, Appl
6	100.0	100.0	356	US-09-807-709A-1	Sequence 759, App
7	100.0	100.0	356	US-09-807-709A-1	Sequence 85983, A
8	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App
9	100.0	100.0	356	US-09-807-709A-1	Sequence 1203, Ap
10	100.0	100.0	356	US-09-807-709A-1	Sequence 23, Appl
11	100.0	100.0	356	US-09-807-709A-1	Sequence 759, App
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18	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App
19	100.0	100.0	356	US-09-807-709A-1	Sequence 1203, Ap
20	100.0	100.0	356	US-09-807-709A-1	Sequence 23, Appl
21	100.0	100.0	356	US-09-807-709A-1	Sequence 759, App
22	100.0	100.0	356	US-09-807-709A-1	Sequence 85983, A
23	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App
24	100.0	100.0	356	US-09-807-709A-1	Sequence 1203, Ap
25	100.0	100.0	356	US-09-807-709A-1	Sequence 23, Appl
26	100.0	100.0	356	US-09-807-709A-1	Sequence 759, App
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28	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App
29	100.0	100.0	356	US-09-807-709A-1	Sequence 1203, Ap
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33	100.0	100.0	356	US-09-807-709A-1	Sequence 178, App

ALIGNMENTS

RESULT 1
US-09-807-709A-1
; Sequence 1, Application US/09807709A
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER
; FILE REFERENCE: 113308-002
; CURRENT APPLICATION NUMBER: US/09/807,709A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP99/07911
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP98203501.6
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-709A-1

Query Match 100.0%; Score 1840; DB 23; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.1e-161;

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160326
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115793C.1.pap
US-10-424-599-160326

Search completed: October 4, 2004, 17:06:09
Job time : 134 secs

Query Match
Best Local Similarity 16.0%; Score 295; DB 12; Length 75;
Matches 52; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 20 TTPPECELDDEDFRCVCFSEFQDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDA 75
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RESULT 14
US-10-240-403-2
; Sequence 2, Application US/10240403
; Publication No. US20040092712A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-403-2

Query Match
Best Local Similarity 13.4%; Score 247; DB 16; Length 47;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 LEQVPKGLPAKLRVLDLSCNRLNRAPODPEVDNLTLDGNPFLVP 315
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RESULT 15
US-10-432-236-2
; Sequence 2, Application US/10432236
; Publication No. US20040091478A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji
; APPLICANT: SHIRAKAWA, Kamon
; APPLICANT: MORI, Sadao
; TITLE OF INVENTION: ANTI CD14 MONOCLONAL ANTIBODY HAVING AN EFFECT OF INHIBITING CD14
; TITLE OF INVENTION: BINDING
; FILE REFERENCE: 1110-0315P
; CURRENT APPLICATION NUMBER: US/10/432,236
; CURRENT FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: human
US-10-432-236-2

Query Match
Best Local Similarity 13.4%; Score 247; DB 16; Length 47;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 198 SDNPELGERGLISALCPLKFPFTLQVIALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 257
QY 243 RATVNPSPRCWMSALNSLNSPAGLEQVPGKLPKLVLDLSCNRLNRAPODELPEV 302
Db 258 RDA--GAPSCDWPQSLNSLNSFTGLKQVPKGLPAKLVLDLSYNRLNRPSPDELPOV 315
QY 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSTLVLLQARGF 355
Db 316 GNLSLKGNPFL---DSSESHSEKFNKSVVVTAGAPSSQVVALSGTLALLGDRLF 365

RESULT 10
US-10-281-478-10
; Sequence 10, Application US/10281478
; Publication No. US20030108959A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Johnson, Richard S.
; APPLICANT: Guo, Lin
; APPLICANT: Mahimkar, Rajeev M.
; APPLICANT: Peschon, Jacques J.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED PROTEINS
; FILE REFERENCE: 3327-A
; CURRENT APPLICATION NUMBER: US/10/281,478
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-281-478-10

Query Match 61.8%; Score 1136.5; DB 14; Length 366;
Best Local Similarity 65.7%; Pred. No. 5e-101;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
QY 3 PEPCELDEDFRCVCFNPFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADPRQ 62
Db 20 PEPCELDEES--CSCNFDKPKDMSAFNCLGADVELYGGRSLEYLLKRVDEADLQ 77
QY 63 YADVTKALVRRITVGAQVPAQLVGCALRVLAYSRKELTLEDKLTGTMPPLLEATG 122
Db 78 FTDIKSLKRLTVRAIRPSRLFGALRVIGISGLQELTLENLEVTGTAPPLLEATG 137
QY 123 LAISLRLNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSEYQVRAFPALTSIDL 182
Db 138 PDNLNLRNVSWATRDWLAELQWLKPKGLKVLISIAQAHSLNFSCEQVRVFPALSTLDL 197
QY 183 SDNPELGERGLISALCPLKFPFTLQVIALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 242
Db 198 SDNPELGERGLISALCPLKFPFTLQVIALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 257
QY 243 RATVNPSPRCWMSALNSLNSPAGLEQVPGKLPKLVLDLSCNRLNRAPODELPEV 302
Db 258 RDA--GAPSCDWPQSLNSLNSFTGLKQVPKGLPAKLVLDLSYNRLNRPSPDELPOV 315
QY 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSTLVLLQARGF 355
Db 316 GNLSLKGNPFL---DSSESHSEKFNKSVVVTAGAPSSQVVALSGTLALLGDRLF 365

RESULT 11
US-10-029-386-30234
; Sequence 30234, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/029,386

; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30234
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHES.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P08571, EVALUATE 2.00e-48
US-10-029-386-30234

Query Match 26.0%; Score 478; DB 14; Length 92;
Best Local Similarity 98.9%; Pred. No. 3.3e-38;
Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 131 RNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSEYQVRAFPALTSIDLSDNPGJGE 190
Db 1 RNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSEYQVRAFPALTSIDLSDNPGJGE 60
QY 191 RGLMAALCPHKFPFAIQNLALRNTGMTPTGVC 222
Db 61 RGLMAALCPHKFPFAIQNLALRNTGMTPTGVC 92

RESULT 12
US-10-131-433-7
; Sequence 7, Application US/10131433
; Publication No. US20030054422A1
; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Lapine
US-10-131-433-7

Query Match 16.9%; Score 310.5; DB 14; Length 59;
Best Local Similarity 96.7%; Pred. No. 2.8e-22;
Matches 58; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 TTTPCELDDEDFRCVCFNPFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADPR 60
Db 1 TTTPCELDDEDFRCVCFNPFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRV-ADADP 59

RESULT 13
US-10-424-599-160326
; Sequence 160326, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

```
Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQAR 389
RESULT 7
US-10-251-718-1
; Sequence 1, Application US/10251718
; Publication No. US20030114377A1
; GENERAL INFORMATION:
; APPLICANT: Kirikland, Theo N.
; APPLICANT: Viriyakosol, Suganya
; TITLE OF INVENTION: Inhibition therapy for septic shock with mutant CD14
; FILE REFERENCE: 6627-PA8068
; CURRENT APPLICATION NUMBER: US/10/251,718
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (326)..(339)
; OTHER INFORMATION: residues are contributed by linker and vector
US-10-251-718-1

Query Match 88.8%; Score 1633; DB 14; Length 339;
Best Local Similarity 97.3%; Pred. No. 4.2e-149;
Matches 319; Conservative 1; Mismatches 6; Indels 2; Gaps 2;

QY 1 TTEPCELDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTEPCELDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLEATG 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLEATG 120
QY 121 TGLSSLRRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSFAPSYEQVRAFPALTS 180
Db 121 TGLSSLRRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSFAPSYEQVRAFPALTS 180
QY 181 DLSNPGLGERGLMAALCPHK-FAIIONLAL-RNTGNETPTGVCALAAAGVQPHSLDLS 238
Db 181 DLSNPGLGERGLMAALFPHKPPFAIIONLALPRNTGNETPTGVCALAAAGVQPHSLDLS 240
QY 239 HNSLRATVNSAPRCMWSLSNLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODE 298
Db 241 HNSLRATVNSAPRCMWSLSNLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODE 300
QY 299 LPEVDNLTLDGNPFLVPGTALPHEGSMN 326
Db 301 LPEVDNLTLDGNPFLVPGTALPHEGERP 328

RESULT 8
US-09-870-759-72
; Sequence 72, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1

QY 3 PEPCELDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 62
Db 20 PEPCELDEES--CSCNFPDQWSEAFNCLGAADVLYGGGRSLEYLLKRVDTADLQ 77
QY 63 YADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLEATG 122
Db 78 FTDIISLSLKLTVRAAIPSRILFGALRVLGISGLQELTLENLEVTGAPPPLLEATG 137
QY 123 LALSSLRRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSFAPSYEQVRAFPALTS 182
Db 138 PDNLINLRNVSWATRDAMLAEQWLKPLKVLISIAQAHSNLFSCFQVRAFPALSTLD 197
QY 183 SDNPGGLGERGLMAALCPHKFAIIONLALRNTGNETPTGVCALAAAGVQPHSLDLS 242
Db 198 SDNPGGLGERGLISALCPKFFTLQVLARNAGMETPGVCALAAARVOLQGLDLSHNSL 257
QY 243 RATVNSAPRCMWSLSNLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODEP 302
Db 258 RDA--GAPSCDWPQLNSLNSFTGLKQVPGKLPKLRVLDLSCNRLNRAPODEP 315
QY 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGF 355
Db 316 GNLSLKGNPFL--DSSEHSEKFNKSVVTVAGAPSSQVALSGTLLALLGDLRF 365

RESULT 9
US-09-751-708A-72
; Sequence 72, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 72
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-72

Query Match 61.8%; Score 1136.5; DB 10; Length 366;
Best Local Similarity 65.7%; Pred. No. 5e-101;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

QY 3 PEPCELDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 62
Db 20 PEPCELDEES--CSCNFPDQWSEAFNCLGAADVLYGGGRSLEYLLKRVDTADLQ 77
QY 63 YADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLEATG 122
Db 78 FTDIISLSLKLTVRAAIPSRILFGALRVLGISGLQELTLENLEVTGAPPPLLEATG 137
QY 123 LALSSLRRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSFAPSYEQVRAFPALTS 182
Db 138 PDNLINLRNVSWATRDAMLAEQWLKPLKVLISIAQAHSNLFSCFQVRAFPALSTLD 197
QY 183 SDNPGGLGERGLMAALCPHKFAIIONLALRNTGNETPTGVCALAAAGVQPHSLDLS 242
Db 198 SDNPGGLGERGLISALCPKFFTLQVLARNAGMETPGVCALAAARVOLQGLDLSHNSL 257
QY 243 RATVNSAPRCMWSLSNLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODEP 302
Db 258 RDA--GAPSCDWPQLNSLNSFTGLKQVPGKLPKLRVLDLSCNRLNRAPODEP 315
QY 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGF 355
Db 316 GNLSLKGNPFL--DSSEHSEKFNKSVVTVAGAPSSQVALSGTLLALLGDLRF 365
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; TYPE: PRT
; ORGANISM: human
US-10-432-236-1

Query Match          99.3%; Score 1827; DB 16; Length 356;
Best Local Similarity 99.4%; Pred. No. 7.8e-168;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60

QY 61 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 120
Db 61 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 120

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 180
Db 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 180

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300

QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 356
Db 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 356

RESULT 5
US-09-925-302-485
; Sequence 485, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (263)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-485

Query Match          98.2%; Score 1807; DB 9; Length 431;
Best Local Similarity 99.2%; Pred. No. 8.8e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 37 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 96

QY 61 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 120
Db 97 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 156

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 180
Db 157 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 216

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 217 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 276

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 277 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 336

QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 353
Db 377 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 389
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QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 180
Db 157 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 216

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 217 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 276

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 277 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 336

QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 353
Db 377 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 389

RESULT 6
US-09-925-302-485
; Sequence 485, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (263)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-485

Query Match          98.2%; Score 1807; DB 12; Length 431;
Best Local Similarity 99.2%; Pred. No. 8.8e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 37 TTPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 96

QY 61 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 120
Db 97 RYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLPLEA 156

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 180
Db 157 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFATSCQVRAFPALTSL 216

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 217 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 276

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 277 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 336

QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 353
Db 377 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 389
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QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db |||||
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db |||||
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db |||||
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db |||||
RESULT 2
US-10-207-655-178
; Sequence 178, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 178
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-178

Query Match 99.5%; Score 1831; DB 14; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.4e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTPEPCLEDDERFCVNCNFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCLEDDERFCVNCNFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDKITGTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDKITGTMPPLPLEA 139
QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLKVLSTIAQHSFAPSYEQVRAPPALTSL 180
Db 140 TGLALSSLRNRVSWATGRSWLAELQWLKPLKVLSTIAQHSFAPSYEQVRAPPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 3
US-10-331-496A-23
; Sequence 23, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 23
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-23

Query Match 99.5%; Score 1831; DB 15; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.4e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTPEPCLEDDERFCVNCNFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCLEDDERFCVNCNFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDKITGTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDKITGTMPPLPLEA 139
QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLKVLSTIAQHSFAPSYEQVRAPPALTSL 180
Db 140 TGLALSSLRNRVSWATGRSWLAELQWLKPLKVLSTIAQHSFAPSYEQVRAPPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 4
US-10-432-236-1
; Sequence 1, Application US/10432236
; Publication No. US20040091478A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji
; APPLICANT: SHIRAKAWA, Kamon
; APPLICANT: MORI, Sadao
; TITLE OF INVENTION: ANTI CD14 MONOCLONAL ANTIBODY HAVING AN EFFECT OF INHIBITING CD14/
; TITLE OF INVENTION: BINDING
; FILE REFERENCE: 1110-0315P
; CURRENT APPLICATION NUMBER: US/10/432,236
; CURRENT FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 1
; LENGTH: 356

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:54:27 ; Search time 131 Seconds
(without alignments)
874.508 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTPECELDDEDFRCVNFCS.....TSLVGVSGTLVLQARGFA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues
Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1831	99.5	356	US-10-240-403-1	Sequence 1, Appli
2	1831	99.5	375	US-10-207-655-178	Sequence 178, App
3	1831	99.5	375	US-10-331-496A-23	Sequence 23, Appl
4	1827	99.3	356	US-10-432-236-1	Sequence 1, Appli
5	1807	98.2	431	US-09-925-302-485	Sequence 485, App
6	1807	98.2	431	US-09-925-302-485	Sequence 485, App
7	1633	88.8	339	US-10-251-718-1	Sequence 1, Appli
8	1136.5	61.8	366	US-09-870-759-72	Sequence 72, Appl
9	1136.5	61.8	366	US-09-751-708A-72	Sequence 10, Appl
10	1136.5	61.8	366	US-10-281-478-10	Sequence 30234, A
11	478	26.0	92	US-10-029-386-30234	Sequence 7, Appli
12	310.5	16.9	59	US-10-131-433-7	Sequence 160326,
13	295	16.0	75	US-10-424-599-160326	Sequence 2, Appli
14	247	13.4	47	US-10-240-403-2	Sequence 2, Appli
15	247	13.4	47	US-10-432-236-2	Sequence 2, Appli

16	152	8.3	971	16	US-10-437-963-116887	Sequence 116887,
17	150	8.2	1128	16	US-10-437-963-179464	Sequence 179464,
18	148.5	8.1	733	16	US-10-437-963-200675	Sequence 200675,
19	148	8.0	702	12	US-10-425-114-45322	Sequence 45322, A
20	147.5	8.0	784	10	US-09-950-041-4	Sequence 4, Appli
21	147.5	8.0	784	12	US-10-456-947-46	Sequence 46, Appli
22	147.5	8.0	784	13	US-10-145-014-23	Sequence 23, Appl
23	147.5	8.0	784	14	US-10-095-627-12	Sequence 12, Appl
24	147.5	8.0	784	16	US-10-732-563-4	Sequence 4, Appli
25	144.5	7.9	353	10	US-09-759-130B-193	Sequence 193, App
26	144.5	7.9	353	10	US-09-946-374-397	Sequence 397, App
27	144.5	7.9	353	11	US-09-833-245-99	Sequence 99, Appl
28	144.5	7.9	353	11	US-09-833-245-100	Sequence 100, App
29	144.5	7.9	353	12	US-10-006-485A-397	Sequence 397, App
30	144.5	7.9	353	12	US-10-013-907A-397	Sequence 397, App
31	144.5	7.9	353	12	US-10-015-499A-397	Sequence 397, App
32	144.5	7.9	353	12	US-10-013-910A-397	Sequence 397, App
33	144.5	7.9	353	12	US-10-226-254A-397	Sequence 397, App
34	144.5	7.9	353	12	US-10-015-395A-397	Sequence 397, App
35	144.5	7.9	353	14	US-10-006-856A-397	Sequence 397, App
36	144.5	7.9	353	14	US-10-006-818A-397	Sequence 397, App
37	144.5	7.9	353	14	US-10-015-393A-397	Sequence 397, App
38	144.5	7.9	353	14	US-10-015-869A-397	Sequence 397, App
39	144.5	7.9	353	14	US-10-012-121A-397	Sequence 397, App
40	144.5	7.9	353	14	US-10-006-116A-397	Sequence 397, App
41	144.5	7.9	353	14	US-10-006-117A-397	Sequence 397, App
42	144.5	7.9	353	14	US-10-017-527A-397	Sequence 397, App
43	144.5	7.9	353	14	US-10-013-913A-397	Sequence 397, App
44	144.5	7.9	353	14	US-10-007-194A-397	Sequence 397, App
45	144.5	7.9	353	14	US-10-013-430A-397	Sequence 397, App

ALIGNMENTS

RESULT 1
US-10-240-403-1
; Sequence 1, Application US/10240403
; Publication NO. US20040092712A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-403-1

Query Match 99.5%; Score 1831; DB 16; Length 356;
Best Local Similarity 99.7%; Pred. No. 3.2e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	TTPECELDDEDFRCVNFSEPODKSEAFQCVSAVEVEHAGGLNLEPFLKRVDAADP	60
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Qy	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKLKELTLEDLKITGTMPPLPLEA	120
Db	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKLKELTLEDLKITGTMPPLPLEA	120
Qy	121	TGALSSLRUNVSWATGRNLAELQWLKPGKVLVSLIAQAHSPAFSYEQVRAPPAITSL	180
Db	121	TGALSSLRUNVSWATGRNLAELQWLKPGKVLVSLIAQAHSPAFSYEQVRAPPAITSL	180
Qy	181	DLSDNPGGLGERGLMAALCPHKFPAIONLALRNTGMTPTGVCALAAGVQPHSLDLSHN	240
Db	181	DLSDNPGGLGERGLMAALCPHKFPAIONLALRNTGMTPTGVCALAAGVQPHSLDLSHN	240

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us-09-807-709d-1.rai

Wed Oct 6 09:56:25 2004

Job time : 35 secs

RESULT 14

US-08-746-883-4
 ; Sequence 4, Application US/08746883
 ; Patent No. 603693
 ; GENERAL INFORMATION:
 ; APPLICANT: Julius, Michael H., Filipp, Dominic,
 ; APPLICANT: Alizadeh-Khavi, Kamel
 ; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
 ; TITLE OF INVENTION: PROTEIN (CD14), ENCODING GENE AND APPLICATION
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/746,883
 ; FILING DATE: No. 6093693ember 18, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 47841/00008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 373 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-746-883-4

Query Match 72.2%; Score 1328.5; DB 3; Length 373;
 Best Local Similarity 74.2%; Pred. No. 1.6e-130;
 Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
 QY 2 TPEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEIHAAGLNLPFLKRVVDADPR 61
 Db 22 TTEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEIHAAGLNLPFLKRVVDADPR 61
 QY 62 QYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAYSKELTLEDKITGMPPLEAT 121
 Db 80 QYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAYSKELTLEDKITGMPPLEAT 121
 QY 122 GLALSSRLRNVSATGRSWLAELQOWLPKGLVLSIAQAHSAPFSYEQVRAFPALTSLD 181
 Db 140 GPALTITSLRNVSATGRSWLAELQOWLPKGLVLSIAQAHSAPFSYEQVRAFPALTSLD 181
 QY 182 LSDNPGGLGERGLMAALCPHKFPALQNLALRNVTGMPETPTGVCAALAAAGVOPHSLSLHNS 241
 Db 200 LSDNPGGLGERGLMAALCPHKFPALQNLALRNVTGMPETPTGVCAALAAAGVOPHSLSLHNS 241
 QY 242 LRATVNPSPAPRCWMSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNLRNRAFPQDELPE 301
 Db 260 LRVTAPGATRCVMPALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNLRNRAFPQDELPE 301
 QY 302 VDNLTLDGNPFVPGTALPHEGS-MNSGVVPACARSTLSVGVSGTLVLQGGARGFA 356
 Db 319 VNDLTLDGNPFVPGTALPHEGS-MNSGVVPACARSTLSVGVSGTLVLQGGARGFA 373

RESULT 15

US-09-313-177-4
 ; Sequence 4, Application US/09313177
 ; Patent No. 6676985

; GENERAL INFORMATION:
 ; APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
 ; APPLICANT: ALIZADEH-KHIAVI, Kamel
 ; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
 ; TITLE OF INVENTION: PROTEIN (CD14), ENCODING GENE AND APPLICATION
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/313,177
 ; FILING DATE: May 18, 1999
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/746,883
 ; FILING DATE: No. 6676985ember 18, 1996
 ; APPLICATION NUMBER: PCT/CA 97/00880
 ; FILING DATE: No. 6676985ember 18, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 47841/00047
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 373 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-313-177-4

Query Match 72.2%; Score 1328.5; DB 4; Length 373;
 Best Local Similarity 74.2%; Pred. No. 1.6e-130;
 Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
 QY 2 TPEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEIHAAGLNLPFLKRVVDADPR 61
 Db 22 TTEPCELDDEDFRCVNFSEPOPDWSEAFQCVSAVEIHAAGLNLPFLKRVVDADPR 61
 QY 62 QYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAYSKELTLEDKITGMPPLEAT 121
 Db 80 QYADTVKALVRRLTVGAQAQVPAQLLVGALRVLAYSKELTLEDKITGMPPLEAT 121
 QY 122 GLALSSRLRNVSATGRSWLAELQOWLPKGLVLSIAQAHSAPFSYEQVRAFPALTSLD 181
 Db 140 GPALTITSLRNVSATGRSWLAELQOWLPKGLVLSIAQAHSAPFSYEQVRAFPALTSLD 181
 QY 182 LSDNPGGLGERGLMAALCPHKFPALQNLALRNVTGMPETPTGVCAALAAAGVOPHSLSLHNS 241
 Db 200 LSDNPGGLGERGLMAALCPHKFPALQNLALRNVTGMPETPTGVCAALAAAGVOPHSLSLHNS 241
 QY 242 LRATVNPSPAPRCWMSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNLRNRAFPQDELPE 301
 Db 260 LRVTAPGATRCVMPALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNLRNRAFPQDELPE 301
 QY 302 VDNLTLDGNPFVPGTALPHEGS-MNSGVVPACARSTLSVGVSGTLVLQGGARGFA 356
 Db 319 VNDLTLDGNPFVPGTALPHEGS-MNSGVVPACARSTLSVGVSGTLVLQGGARGFA 373

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RESULT 12
US-08-484-397A-2
; Sequence 2, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-397A-2

Query Match 95.8%; Score 1762; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 6e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTTPFCBLDDDFRCVCFNFPDWSFAFCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 1 TTTPFCGGGDDDFRCVCFNFPDWSFAFCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
DB 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
QY 121 TGLALSSLRNLNVSATGRSLAELOQWLKPLKVLSTAOAHSPAFSVEQVRAPFALTSL 180
DB 121 TGLALSSLRNLNVSATGRSLAELOQWLKPLKVLSTAOAHSPAFSVEQVRAPFALTSL 180
QY 181 DLSNPGGLGERGLMAALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSNPGGLGERGLMAALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOQDELP 300
DB 241 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOQDELP 300
QY 301 EVDNLTLDGNPFLVPGTALPHGSMNSGVVPACARSTLSVGVSGTLVL 348

DB 301 EVDNLTLDGNPFLVPGTALPHGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 13
US-08-484-397A-8
; Sequence 8, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-397A-8

Query Match 92.9%; Score 1710; DB 2; Length 334;
Best Local Similarity 99.7%; Pred. No. 1.6e-170;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CVCNFPDQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVDAADPQYADTVKALRVRR 74
DB 1 CVCNFPDQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVDAADPQYADTVKALRVRR 60
QY 75 LTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEATGLALSSLRNVS 134
DB 61 LTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEATGLALSSLRNVS 120
QY 135 WATGRSLAELOQWLKPLKVLSTAOAHSPAFSVEQVRAPFALTSLDSDNPGGLGERGLM 194
DB 121 WATGRSLAELOQWLKPLKVLSTAOAHSPAFSVEQVRAPFALTSLDSDNPGGLGERGLM 180
QY 195 AALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHNSLRATVNSAPRCM 254
DB 191 AALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHNSLRATVNSAPRCM 240
QY 255 WSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOQDELPVDNLTLDGNPFLV 314
DB 241 WSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOQDELPVDNLTLDGNPFLV 300
QY 315 PGTALPHGSMNSGVVPACARSTLSVGVSGTLVL 348
DB 301 PGTALPHGSMNSGVVPACARSTLSVGVSGTLVL 348

QY 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
DB 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 10

US-08-484-397A-5
; Sequence 5, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-5

Query Match 95.8%; Score 1763; DB 2; Length 348;
Best Local Similarity 98.9%; Pred. No. 4.7e-176;
Matches 344; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTPEPCBLDEDFRCVCFNFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 1 TTPEPCBLLEDFRCVCFNFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPPLEA 120
DB 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPPLEA 120
QY 121 TGLALSLRLNYSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
DB 121 TGLALSLRLNYSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300

DB 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 11

US-08-484-397A-6
; Sequence 6, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-6

Query Match 95.8%; Score 1763; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 4.7e-176;
Matches 343; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTPEPCBLDEDFRCVCFNFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 1 TTPEPCBLLEDFRCVCFNFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPPLEA 120
DB 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPPLEA 120
QY 121 TGLALSLRLNYSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
DB 121 TGLALSLRLNYSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSNDPGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
DB 241 SLRATVNSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300

QY 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNPSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSNRLNRAFPQDPDLP 300
DB 241 SLRATVNPSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSNRLNRAFPQDPDLP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVVPACARSTLSVGSGLTLLV 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVVPACARSTLSVGSGLTLLV 348

RESULT 8
US-08-484-397A-7
; Sequence 7, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/484.397A
; APPLICATION NUMBER: US/08/484.397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cury, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-7

Query Match 95.9%; Score 1764; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 3.7e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTPPECELDDEDFRCVCFNPFSEPPQDSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
DB 1 TTPPECPPEPPDFRCVCFNPFSEPPQDSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
QY 61 ROYADVTKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEA 120
DB 61 ROYADVTKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEA 120
QY 121 TGLALSSRLRNVSWATGRSWLAELQOQWLKPGIKVLSIAQAHSAPFSCQVRAFPALTSL 180
DB 121 TGLALSSRLRNVSWATGRSWLAELQOQWLKPGIKVLSIAQAHSAPFSCQVRAFPALTSL 180
QY 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240

DB 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNPSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSNRLNRAFPQDPDLP 300
DB 241 SLRATVNPSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSNRLNRAFPQDPDLP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVVPACARSTLSVGSGLTLLV 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVVPACARSTLSVGSGLTLLV 348

RESULT 9
US-08-484-397A-4
; Sequence 4, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/484.397A
; APPLICATION NUMBER: US/08/484.397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cury, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-4

Query Match 95.8%; Score 1763; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 4.7e-176;
Matches 343; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTPPECELDDEDFRCVCFNPFSEPPQDSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
DB 1 TTPPECVVVEDFRCVCFNPFSEPPQDSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
QY 61 ROYADVTKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEA 120
DB 61 ROYADVTKALRVRLTVGAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEA 120
QY 121 TGLALSSRLRNVSWATGRSWLAELQOQWLKPGIKVLSIAQAHSAPFSCQVRAFPALTSL 180
DB 121 TGLALSSRLRNVSWATGRSWLAELQOQWLKPGIKVLSIAQAHSAPFSCQVRAFPALTSL 180
QY 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSDFPGLGERGLMAALCPHKFPAIQNLALRNTGMPETPTGVCALAAAGVQPHSLDLSHN 240

Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDDEL 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 6
US-08-484-397A-38
; Sequence 38 Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..10
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Xaa is independently selected from Gly, Ala, Val, Leu"
; OTHER INFORMATION: Ile and Pro"
US-08-484-397A-38

Query Match 96.0%; Score 1766; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 2.3e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCXXXDDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
Db 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
Qy 121 TGLALSSLRNLSRVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180

Db 121 TGLALSSLRNLSRVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDDEL 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 7
US-08-484-397A-3
; Sequence 3, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-3

Query Match 95.9%; Score 1764; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 3.7e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCAAAADDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
Db 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
Qy 121 TGLALSSLRNLSRVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Db 121 TGLALSSLRNLSRVSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180

Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 139
QY 121 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 140 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 199
QY 181 DLSDNPGGLGRGLMAALCPHKFPAIONLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSDNPGGLGRGLMAALCPHKFPAIONLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKRLVLDLSCNRLNRAFPQDDEL 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKRLVLDLSCNRLNRAFPQDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQARGFA 375

RESULT 4

US-08-366-953A-45
; Sequence 45, Application US/08366953A
; Patent No. 5766593
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 PEPTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,953A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook Ph.D., Robert R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-324
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-366-953A-45

Query Match 97.3%; Score 1791; DB 1; Length 348;
Best Local Similarity 99.7%; Pred. No. 5.5e-179;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEFPQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCELDEDFRCVNFSEFPQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
QY 121 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 121 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 180

QY 181 DLSDNPGGLGRGLMAALCPHKFPAIONLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSDNPGGLGRGLMAALCPHKFPAIONLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKRLVLDLSCNRLNRAFPQDDEL 300
Db 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKRLVLDLSCNRLNRAFPQDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLL 348

RESULT 5

US-08-484-397A-27
; Sequence 27, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1030
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-27

Query Match 97.3%; Score 1791; DB 2; Length 348;
Best Local Similarity 99.7%; Pred. No. 5.5e-179;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEFPQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCELDEDFRCVNFSEFPQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
QY 121 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 121 TGLALSLRLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSPAFSVEQVRAPPAITSL 180
QY 181 DLSDNPGGLGRGLMAALCPHKFPAIONLALRNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240

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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:51:31 ; Search time 32 Seconds
(without alignments)
574.339 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPEPCELDEDFRCVNFNS.....TLGVGVSGTLVLLQGARGFA 356

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*

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6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	100.0	375	US-08-746-883-5	Sequence 5, Appl
2	1840	100.0	375	US-09-313-177-5	Sequence 5, Appl
3	1826	99.2	375	US-08-205-719-2	Sequence 2, Appl
4	1791	97.3	348	US-08-366-953A-45	Sequence 45, Appl
5	1791	97.3	348	US-08-484-397A-27	Sequence 27, Appl
6	1766	96.0	348	US-08-484-397A-38	Sequence 38, Appl
7	1764	95.9	348	US-08-484-397A-3	Sequence 3, Appl
8	1764	95.9	348	US-08-484-397A-7	Sequence 7, Appl
9	1763	95.8	348	US-08-484-397A-4	Sequence 4, Appl
10	1763	95.8	348	US-08-484-397A-5	Sequence 5, Appl
11	1763	95.8	348	US-08-484-397A-6	Sequence 6, Appl
12	1762	95.8	348	US-08-484-397A-2	Sequence 2, Appl
13	1710	92.9	334	US-08-484-397A-8	Sequence 8, Appl
14	1328.5	72.2	373	US-08-746-883-4	Sequence 4, Appl
15	1328.5	72.2	373	US-09-313-177-4	Sequence 4, Appl
16	1136.5	61.8	366	US-08-746-883-6	Sequence 6, Appl
17	1136.5	61.8	366	US-09-313-177-6	Sequence 6, Appl
18	765	41.6	152	US-08-484-397A-10	Sequence 10, Appl
19	765	41.6	152	US-08-484-397A-14	Sequence 14, Appl
20	764	41.5	152	US-08-484-397A-11	Sequence 11, Appl
21	764	41.5	152	US-08-484-397A-12	Sequence 12, Appl
22	764	41.5	152	US-08-484-397A-13	Sequence 13, Appl
23	763	41.5	152	US-08-484-397A-9	Sequence 9, Appl
24	711	38.6	138	US-08-484-397A-15	Sequence 15, Appl
25	334	18.2	60	US-08-484-397A-28	Sequence 28, Appl
26	320	17.4	60	US-08-484-397A-34	Sequence 34, Appl
27	316	17.2	60	US-08-484-397A-37	Sequence 37, Appl

28	311	16.9	60	2	US-08-484-397A-33	Sequence 33, Appl
29	310	16.8	60	2	US-08-484-397A-35	Sequence 35, Appl
30	309	16.8	60	2	US-08-484-397A-31	Sequence 31, Appl
31	307	16.7	55	1	US-08-366-953A-36	Sequence 36, Appl
32	307	16.7	60	2	US-08-484-397A-29	Sequence 29, Appl
33	307	16.7	60	2	US-08-484-397A-36	Sequence 36, Appl
34	306	16.6	60	2	US-08-484-397A-30	Sequence 30, Appl
35	304	16.5	60	2	US-08-484-397A-32	Sequence 32, Appl
36	284	15.4	55	1	US-08-366-953A-41	Sequence 41, Appl
37	283	15.4	55	1	US-08-366-953A-42	Sequence 42, Appl
38	283	15.4	55	1	US-08-366-953A-43	Sequence 43, Appl
39	282	15.3	55	1	US-08-366-953A-39	Sequence 39, Appl
40	280	15.2	55	1	US-08-366-953A-37	Sequence 37, Appl
41	280	15.2	55	1	US-08-366-953A-44	Sequence 44, Appl
42	279	15.2	55	1	US-08-366-953A-38	Sequence 38, Appl
43	277	15.1	55	1	US-08-366-953A-40	Sequence 40, Appl
44	147.5	8.0	784	4	US-09-982-308B-23	Sequence 23, Appl
45	128	7.0	1196	3	US-08-881-706-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-746-883-5
; Sequence 5, Application US/08746883
; Patent No. 6093693
; GENERAL INFORMATION:
; APPLICANT: Julius, Michael H., Philipp, Dominic,
; APPLICANT: Alizadeh-Khiavi, Kamel
; TITLE OF INVENTION: B Cell Activation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,883
; FILING DATE: No. 6093693ember 18, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 47841/00008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-746-883-5

Query Match 100.0%; Score 1840; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTPEPCELDEDFRCVNFSEFPQDWSAEFQCVSAVEVEIHAGGLNLEPFLKRVADADP	60
Db	20	TTPEPCELDEDFRCVNFSEFPQDWSAEFQCVSAVEVEIHAGGLNLEPFLKRVADADP	79
QY	61	RQYADTVKALRVRLITVGAQVPAQLLVGALRVLAYSRKLKELTLEDLKITGTMPPLPLEA	120
Db	80	RQYADTVKALRVRLITVGAQVPAQLLVGALRVLAYSRKLKELTLEDLKITGTMPPLPLEA	139

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GENERAL INFORMATION:
APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
ALIZADEH-KHIAVI, Kamei
TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
PROTEIN (CD14), ENCODING GENE AND APPLICATION
IN B CELL ACTIVATION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/734,149
FILING DATE: 15-Dec-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/313,177
FILING DATE: 18-May-1999
APPLICATION NUMBER: 08/746,883
FILING DATE: November 18, 1996
APPLICATION NUMBER: PCT/CA 97/00880
FILING DATE: November 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 47841/00047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-734-149-4

Query Match 72.2%; Score 1328.5; DB 6; Length 373;
Best Local Similarity 74.2%; Pred. No. 2.1e-104;
Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
QY 2 TPECELDDEDFRCVCFNFPDQWSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 61
DB 22 TPECELDDEDFRCVCFNFTDPKDWSSAVQWAVEVEISAGRSLSQFLK--GADTNPK 79
QY 62 QYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEAT 121
DB 80 QYADTVKALRVRLKLGAAQVPAQLLVALRGALGYSRKELTLEDLKITGTMPPLPLEA 139
QY 122 GLALSSLRRLNVSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPALTSLD 181
DB 140 GPALTITLSLRNVSWTTGAMLGELQWLKPGKLVLSIAQAHSAPFSYEQVRAPALTSLD 199
QY 182 LSDNPGGLGRLMAALCPHKFPALONALRNTGMEPTGVCAALAAAGVOPHSIDLSHNS 241
DB 200 LSDNPSLGDITGLMAALCPNFKFPALQYALRNAGMETPGVCAALAAARVOPQSLDLSHNS 259
QY 242 LRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOQDELPE 301
DB 260 LRVTAPGATRCVWPSALNSLNSFAGLEQVPGKLPKLSVLDLSCNKLSPRPRDELPE 318
QY 302 VDNLTLDGNPFLVPGTALPHEGS--MNSGVVPACARSTLSVGVSTVLVLLQARGFA 356
DB 319 VDNLTLDGNPFLDPG-ALQCNDFPMISGVVPACARSALTMGVSGALALLQARGFA 373

RESULT 11

US-10-891-105-7
Sequence 7, Application US/10891105
GENERAL INFORMATION:
APPLICANT: JULIUS, Michael H.
APPLICANT: FILIPP, Dominik
TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
TITLE OF INVENTION: LAIT/SCD14-PROTEIN
FILE REFERENCE: 47841/00063
CURRENT APPLICATION NUMBER: US/10/891,105
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US/09/721,904
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: PCT/CA99/00482
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: US 60/086,884
PRIOR FILING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Wordperfect 9.0
SEQ ID NO 7
LENGTH: 377
TYPE: PRT
ORGANISM: rabbit
FEATURE:
NAME/KEY: unsure
LOCATION: (14)
OTHER INFORMATION: Xaa = unknown
FEATURE:
NAME/KEY: unsure
LOCATION: (265)---(267)
OTHER INFORMATION: Xaa = unknown
FEATURE:
NAME/KEY: unsure
LOCATION: (269)
OTHER INFORMATION: Xaa = unknown
US-10-891-105-7

Query Match 72.1%; Score 1326.5; DB 6; Length 377;
Best Local Similarity 72.7%; Pred. No. 3.2e-104;
Matches 258; Conservative 34; Mismatches 62; Indels 1; Gaps 1;
QY 2 TPECELDDEDFRCVCFNFPDQWSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 61
DB 22 TPECELDDEDFRCVCFNFPDQWSSALQCMQVAVQVEMWGGHSLQFLKQADLYTDQR 81
QY 62 QYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPLPLEA 120
DB 82 RYADVVKALRVRLTVGAVQVPAQLLVGLRVGLYSRKELALEDEIVTGTAPPPPLEA 141
QY 121 TGLALSSLRRLNVSWATGRSWLAELQWLKPGKLVLSIAQAHSAPFSYEQVRAPALTSL 180
DB 142 TGPALSTLSLRNVSWPKGAWLSLQWLKPGKLVLSIAQAHSAPFSYEQVRAPALTSL 201
QY 181 DLSNPGGLGRLMAALCPHKFPALONALRNTGMEPTGVCAALAAAGVOPHSIDLSHN 240
DB 202 DLSNPGGLGRLVAAALCPHKFPALQYALRNAGMETPGVCAALAAAGVOPHLLDLSH 261
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOQDELPE 300
DB 262 SLRXXXAXDTCRCIWPSPALNSLNSFTGLQVQVPGKLPKLVLDLSCNKLNRAPQGP 321
QY 301 EVDNLTLDGNPFLVPGTALPHEGS--MNSGVVPACARSTLSVGVSTVLVLLQARGF 355
DB 322 KVNLSLDGNPFLVPGASLQEDLTNSGVTFPACPPSPPLAMGSGTLLALLQARGF 376

RESULT 12

US-10-428-817A-68
Sequence 68, Application US/10428817A
GENERAL INFORMATION:
APPLICANT: TERMAN, David S

;; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001469
;; CURRENT APPLICATION NUMBER: US/60/582,609
;; CURRENT FILING DATE: 2004-06-25
;; NUMBER OF SEQ ID NOS: 97101
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2787
;; LENGTH: 375
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-582-609-2787

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 5e-147;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79

QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
DB 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 139

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 180
DB 140 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259

QY 241 SLRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
DB 260 SLRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 8
US-10-432-236A-1
;; Sequence 1, Application US/10432236A
;; GENERAL INFORMATION:
;; APPLICANT: FURUSAKO, Shoji
;; APPLICANT: SHIRAKAWA, Kamon
;; APPLICANT: MORI, Sadao
;; TITLE OF INVENTION: ANTI CD14 MONOCLONAL ANTIBODY HAVING AN EFFECT OF INHIBITING CD14
;; TITLE OF INVENTION: BINDING
;; FILE REFERENCE: 1110-0315P
;; CURRENT APPLICATION NUMBER: US/10/432,236A
;; CURRENT FILING DATE: 2003-05-22
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 1
;; LENGTH: 356
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-432-236A-1

Query Match 99.3%; Score 1827; DB 6; Length 356;
Best Local Similarity 99.4%; Pred. No. 1e-146;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 1 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60

QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
DB 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 180

DB 121 TGLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 180
QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
DB 241 SLRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356

RESULT 9
US-10-891-105-4
;; Sequence 4, Application US/10891105
;; GENERAL INFORMATION:
;; APPLICANT: JULIUS, Michael H.
;; APPLICANT: FILIPP, Dominik
;; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
;; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
;; FILE REFERENCE: 47841/00063
;; CURRENT APPLICATION NUMBER: US/10/891,105
;; CURRENT FILING DATE: 2004-07-15
;; PRIOR APPLICATION NUMBER: US/09/721,904
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: PCT/CA99/00482
;; PRIOR FILING DATE: 1999-05-27
;; PRIOR APPLICATION NUMBER: US 60/086,884
;; PRIOR FILING DATE: 1998-05-27
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: Wordperfect 9.0
;; SEQ ID NO 4
;; LENGTH: 373
;; TYPE: PRT
;; ORGANISM: bovine
US-10-891-105-4

Query Match 72.2%; Score 1328.5; DB 6; Length 373;
Best Local Similarity 74.2%; Pred. No. 2.1e-104;
Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;

QY 2 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 61
DB 22 TTPPECELDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79

QY 62 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 121
DB 80 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 139

QY 122 GLALSSLRNVSWATGRSWLAELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 181
DB 140 GPALTTLNLSNVSWTTCGAWLGELQWLKPGKLVLSIAQAHSFAPSYEQVRAFPALTSL 199

QY 182 LSDNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 241
DB 200 LSDNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259

QY 242 LRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 301
DB 260 LRATVNPSPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 318

QY 302 VDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
DB 319 VDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 373

RESULT 10
US-10-734-149-4
;; Sequence 4, Application US/10734149

; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-734-149-5

Query Match 100.0%; Score 1840; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 120
DB 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 139
QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 199
QY 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 300
DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 5

PCT-US03-24918A-460

; Sequence 460, Application PC/TUS0324918A

; GENERAL INFORMATION:

; APPLICANT: GENECAST, INC.

; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

; FILE REFERENCE: 49076.000004.PCT2

; CURRENT APPLICATION NUMBER: PCT/US03/24918A

; CURRENT FILING DATE: 2003-07-26

; PRIOR APPLICATION NUMBER: 10/207,655

; PRIOR FILING DATE: 2002-07-25

; PRIOR APPLICATION NUMBER: 10/053,530

; PRIOR FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 60/367,358

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/385,691

; PRIOR FILING DATE: 2002-06-03

; NUMBER OF SEQ ID NOS: 704

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 460

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-24918A-460

Query Match 99.5%; Score 1831; DB 1; Length 375;
Best Local Similarity 99.7%; Pred. No. 5e-147;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 120
DB 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 139

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 199
QY 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 300
DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 6

US-10-170-205E-22096

; Sequence 22096, Application US/10170205E

; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark

; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

; FILE REFERENCE: CL001381

; CURRENT APPLICATION NUMBER: US/10/170,205E

; CURRENT FILING DATE: 2002-06-13

; NUMBER OF SEQ ID NOS: 40312

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 22096

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-170-205E-22096

Query Match

Best Local Similarity 99.7%; Score 1831; DB 6; Length 375;

Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 120
DB 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLEA 139
QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQHSAPFSYEQVRAFPALTSL 199
QY 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMEFTPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 300
DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQHSAPFSYEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 7

US-60-582-609-2787

; Sequence 2787, Application US/60582609

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: HUANG, Hongjin

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,


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RESULT 2
US-09-807-709D-1
; Sequence 1, Application US/09807709D
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER
; FILE REFERENCE: 113308-002
; CURRENT APPLICATION NUMBER: US/09/807,709D
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP99/07911
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP98203501.6
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-709D-1

Query Match      100.0%; Score 1840; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 8.1e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Db 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Qy 121 TGLALSSLRNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSYEQVRAPFALTSL 180
Db 121 TGLALSSLRNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSYEQVRAPFALTSL 180
Qy 181 DLSNPGLGERGLMAALCPHKFPAIONLALNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGLGERGLMAALCPHKFPAIONLALNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAFPQDPELP 300
Db 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAFPQDPELP 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356

RESULT 3
US-10-891-105-5
; Sequence 5, Application US/10891105
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; FILE REFERENCE: 47841/00063
; CURRENT APPLICATION NUMBER: US/10/891,105
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US/09/721,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086,884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Wordperfect 9.0
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
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; ORGANISM: human
US-10-891-105-5

Query Match      100.0%; Score 1840; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
Qy 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Db 80 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 139
Qy 121 TGLALSSLRNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSYEQVRAPFALTSL 180
Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPKGLKVLISIAQAHSPAFSYEQVRAPFALTSL 199
Qy 181 DLSNPGLGERGLMAALCPHKFPAIONLALNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGLGERGLMAALCPHKFPAIONLALNTGMTPTGVCALAAAGVQPHSLDLSHN 259
Qy 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAFPQDPELP 300
Db 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAFPQDPELP 319
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 4
US-10-734-149-5
; Sequence 5, Application US/10734149
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
; PROTEIN (CD14), ENCODING GENE AND APPLICATION
; IN B CELL ACTIVATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,149
; FILING DATE: 15-Dec-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/313,177
; FILING DATE: 18-May-1999
; APPLICATION NUMBER: 08/746,883
; FILING DATE: November 18, 1996
; APPLICATION NUMBER: PCT/CA 97/00880
; FILING DATE: November 18, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 47841/00047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:53:41 ; Search time 74 Seconds
(without alignments)
759.304 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPEPCLEDDDFRCVNF...TLVGSGTLLVQARGGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 838593 seqs, 157832909 residues

Total number of hits satisfying chosen parameters: 838593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1840	100.0	356	US-09-807-709C-1	Sequence 1, Appli
2	1840	100.0	356	US-09-807-709D-1	Sequence 1, Appli
3	1840	100.0	375	US-10-891-105-5	Sequence 5, Appli
4	1840	100.0	375	US-10-734-149-5	Sequence 5, Appli
5	1831	99.5	375	PCT-US03-24918A-460	Sequence 460, App
6	1831	99.5	375	US-10-170-205E-22096	Sequence 22096, A
7	1831	99.5	375	US-60-582-609-2787	Sequence 2787, Ap
8	1827	99.3	356	US-10-432-236A-1	Sequence 1, Appli
9	1328.5	72.2	373	US-10-891-105-4	Sequence 4, Appli
10	1328.5	72.2	373	US-10-734-149-4	Sequence 4, Appli
11	1326.5	72.1	377	US-10-891-105-7	Sequence 7, Appli
12	1136.5	61.8	366	US-10-428-817A-68	Sequence 68, Appl
13	1136.5	61.8	366	US-10-891-105-6	Sequence 6, Appli
14	1136.5	61.8	366	US-10-281-478A-10	Sequence 10, Appl
15	1136.5	61.8	366	US-10-734-149-6	Sequence 6, Appli
16	297	16.1	72	US-10-793-479-4330	Sequence 4330, Ap
17	247	13.4	47	US-10-432-236A-2	Sequence 2, Appli
18	154	8.4	557	US-10-449-902-31160	Sequence 31160, A
19	152	8.3	613	US-10-425-115-277910	Sequence 277910, A
20	147.5	8.0	775	US-10-940-774-8799	Sequence 8799, Ap
21	147.5	8.0	784	US-10-732-796A-4	Sequence 4, Appli
22	147.5	8.0	784	US-10-170-205E-33662	Sequence 33662, A
23	147.5	8.0	784	US-10-760-620A-3558	Sequence 3558, Ap
24	147.5	8.0	784	US-10-760-320A-3558	Sequence 3558, Ap
25	147.5	8.0	784	US-60-582-609-2291	Sequence 2291, Ap
26	144.5	7.9	353	US-09-833-245A-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1

US-09-807-709C-1
; Sequence 1, Application US/09807709C
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER
; FILE REFERENCE: 113308-002
; CURRENT APPLICATION NUMBER: US/09/807,709C
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP99/07911
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP98203501.6
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-709C-1

Query Match	100.0%;	Score 1840;	DB 5;	Length 356;
Best Local Similarity	100.0%;	Pred. No. 8.1e-148;		
Matches	356;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	TTPEPCLEDDDFRCVNFSEPODMSAEFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60	
Db	1	TTPEPCLEDDDFRCVNFSEPODMSAEFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60	
QY	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDIKITGTMPPPLEA	120	
Db	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDIKITGTMPPPLEA	120	
QY	121	TGLALSSLRNVSWATGSRWLAELQWLKPGKVLISIAQAHPSPSYEQVRAFPALTSL	180	
Db	121	TGLALSSLRNVSWATGSRWLAELQWLKPGKVLISIAQAHPSPSYEQVRAFPALTSL	180	
QY	181	DLSDNPLGGERGLMAALCPHKFPAIONLALRNTGMTPTGVCALAAAGVOPHSLDLSHN	240	
Db	181	DLSDNPLGGERGLMAALCPHKFPAIONLALRNTGMTPTGVCALAAAGVOPHSLDLSHN	240	
QY	241	SLRATVNPAPRCMWSALNSLNSFLAGLEQVFKGLPAKLRVLDSLNCNLRNAPQPDLP	300	
Db	241	SLRATVNPAPRCMWSALNSLNSFLAGLEQVFKGLPAKLRVLDSLNCNLRNAPQPDLP	300	
QY	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVQARGGFA	356	
Db	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVQARGGFA	356	